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(54) **Apoptosis-regulating proteins**

(57) Adenovirus E1B 19 kD protein protects against cell death induced by viral infection and certain external physical and chemical stimuli. Activity of the 19 kD protein is similar to the cell death suppressing activity of the protein coded by the Bcl-2 protooncogene. Bcl-2 protein can functionally substitute for the E1B 19 kD protein during adenovirus infection and in transformation of primary cells with adenovirus E1A. Five different cDNA's for proteins, designated Nip1, Nip2, Nip3, Bip1A and Bip13 that specifically interact with the 19 kD protein were found. Mutational analysis of the interaction indicates that at least four of the proteins (Nip1, Nip2, Nip3 and Bip1A) associate with 19 kD protein at specific sites thereof. Homologous motifs are found on Bcl2. An additional protein, (Bip5), interacts with Bcl-2 but not with the 19K protein.

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Description

Apoptosis is a naturally occurring cell death characterized by reduction in cell volume, nuclear condensation, cell blebbing, and endonucleolytic degradation of DNA at nucleosomal intervals. The onset of apoptosis arises from an activation of one or more genetic programs. Apoptosis is distinct from cell necrosis where chromatin clumps, organelles swell and eventually the cell membrane dissolves (Edgington, 1993).

The 19 kD (19K) protein coded by the adenovirus (Ad) E1B region confers a survival function in adenovirus-infected cells and prevents premature cell death. The DNA fragmentation observed in cells infected with E1B 19K mutants is reminiscent of that observed during apoptosis (Wyllie, 1980). Hence, one can infer that the 19 kD protein protects against a cell death program induced by viral infection, thus facilitating efficient virus replication. The E1A proteins, and specifically the conserved region (CR) 1 and CR2 which interact with cellular proteins p300 and pRb and induce cellular proliferation, have been implicated in the onset of the virus-induced death program (White et al., 1991; Mymryk et al., 1994).

The 19 kD protein suppresses the cytotoxic effects of certain external stimuli such as tumor necrosis factor (TNF)- α (Gooding et al., 1991; White et al., 1992) and anti-Fas antibody (Hashimoto et al., 1991). Both TNF- α and anti-Fas have been shown to cause cell death through apoptosis (Laster et al., 1988; Itoh et al., 1991; Watanabe-Fukunaga et al., 1992). Similarly, the 19 kD protein protects cells against the effects of DNA damaging agents such as the anti-cancer drug cisplatin (Subramanian et al., 1993) and UV (Tarodi et al., 1993). Both cisplatin (Sorenson & Eastman, 1988) and UV (reviewed by Williams, 1991) induce cell death through the apoptotic pathway.

Levels of p53 increase in response to DNA damaging agents and it appears that the accumulation of p53 is responsible for the induction of apoptosis by DNA damaging agents (Clarke et al., 1993; Lowe et al., 1993; Lane, 1993). Since 19K can efficiently suppress cell death induced by DNA damaging agents (Subramanian et al., 1993; Tarodi et al., 1993), it appears that 19K suppresses p53-dependent apoptosis (Debbas and White, 1993). Thus, the 19 kD protein provides a survival function in virus-infected cells and also protects cells against certain other cell death-inducing stimuli.

The survival function provided by E1B 19K appears to be strikingly similar to the activity of the cellular proto-oncogene, bcl-2. The bcl-2 oncogene enhances the survival of hematopoietic B and T cells by blocking apoptosis (Vaux et al., 1988; Sentman et al., 1991; Strasser et al., 1991). Overexpression of Bcl-2 protein inhibits apoptosis induced by treatment with glucocorticoids (Ahnemri et al., 1992a), deprivation of cytokines (Nunez et al., 1990; Hockenbery et al., 1990), activation of the c-myc oncogene (Bissonnette et al., 1992; Fanidi et al., 1992), radiation (Strasser et al., 1991) and other DNA damaging agents (Tarodi et al., 1993).

Thus, Bcl-2 appears to protect against apoptosis induced by diverse agents. The effect of the 19 kD protein on cell death induced by such a multitude of stimuli has yet to be examined. However, it is known that the Bcl-2 protein can substitute for the 19 kD protein during adenovirus infection. The characteristic fragmentation of cellular DNA induced by infection with Ad2 19K mutants is suppressed in cells expressing the human Bcl-2 protein (Tarodi et al., 1993). Similarly, expression of Bcl-2 by an adenovirus 2/Bcl-2 recombinant virus does not induce DNA fragmentation in infected cells and forms small plaques on cell monolayers. Rao et al. (1992) reported that Bcl-2 can substitute for 19K, albeit at reduced levels, in transformation of primary rat kidney cells in cooperation with E1A.

Studies have indicated that there are a number of molecules with homology to and that have similar activities with bcl-2. Hence, there might be termed an assemblage of functionally related molecules which includes BHRF-1, bcl-X_L, bcl-X_S, mcl-1 and the like. The similarity can extend to a structural homology at the nucleic acid level, protein level or both. But as will be revealed hereinbelow, the homology need not be over the length of the molecule but can be confined to discrete functional portions of the molecule. Hence, under that criterion, 19K also comprises the assemblage of molecules relating to apoptosis.

The mechanism by which the 19K gene and the Bcl-2 protooncogene protect against cell death is not known. It is possible that those apoptosis-regulating proteins (hereinafter blocking proteins) mediate cell survival by interacting with certain cellular apoptosis-regulating proteins. Identification of any such cellular apoptosis-regulating proteins which interact with E1B 19 kD protein and with Bcl-2 would enable regulation of apoptosis in cells.

An object of the instant invention is to provide proteins, and the nucleic acids encoding said proteins, which bind to proteins known to regulate cell survival.

Another object of the instant invention is to provide oligopeptides, and the nucleic acids encoding said oligopeptides which mediate the interaction between proteins of the instant invention and proteins known to regulate cell survival.

Yet another object of the instant invention is use of said proteins and oligopeptides which bind to proteins known to regulate cell survival in diagnostic assays to assess presence and activity of said cell survival regulating proteins.

In another embodiment, the present invention also encompasses nucleic acid molecules that hybridize to the above-mentioned nucleic acid sequences of the present invention and encode a polypeptide which binds to a site of a molecule which regulates cell survival. The hybridization is under conventional hybridization conditions, preferably under stringent conditions.

The nucleic acid molecule of the present invention can either be DNA or RNA molecules. The invention also encompasses DNA molecules that encode anti-sense RNAs or specific ribozymes which allow the control of the expression of the nucleic acid molecules of the present invention in desired host and target cells. Said anti-sense RNAs and specific ribozymes are also contemplated by the present invention. Furthermore, in another embodiment, the invention relates to primers which allow the specific amplification of nucleic acid molecules of the present invention or of any specific parts thereof. In another embodiment, the invention relates to probes that specifically hybridise to nucleic acid sequences of the present invention or to any part thereof.

In another embodiment, the present invention relates to vectors, comprising said DNA molecule of the present invention. Such vectors are preferably plasmids, cosmids or phage vectors.

In a preferred embodiment of the vector of the present invention, said DNA molecule of the present invention contained therein is operably linked to a promoter.

The promoter is selected so as to allow expression of said DNA molecule in a desired host cell of the present invention.

In another embodiment, the present invention relates to host cells which contain the vector of the present invention. These host cells can be either prokaryotic or eucaryotic. An example of preferred prokaryotic host cells are bacteria such as those of the genus *Escherichia*. Examples of preferred eucaryotic cells are yeast or animal cells.

The polypeptide of the invention may be produced by culturing a host cell of the invention and recovering from said culture the polypeptide so produced.

In another embodiment, the present invention relates to pharmaceutical and diagnostic compositions comprising the nucleic acid molecules, the polypeptides or the oligopeptides of the present invention.

Those and other objects have been achieved in the identification of a series of proteins which bind to the E1B 19K and Bcl-2 proteins, and in the identification of consensus sequences shared by the proteins which mediate the binding therebetween.

Figure 1 depicts the functional organization of the 19 kD protein. The 19 kD sequences involved in suppression of cisplatin-induced cell death and E1A-cooperative transformation are based on Subramanian et al. (1993). In the top half of the figure, solid line bars indicate strong effects of various mutants on the 19 kD functions and interaction with cellular proteins, bars with dashed lines indicate weak effects. The sequence similarity between the 19 kD and Bcl-2 proteins and the mutants that map within those sequences (set off in boxes) are shown at the bottom of the figure (residues 50-56 of SEQ ID NO:8, residues 90-98 of SEQ ID NO:8, residues 106-112 of SEQ ID NO:16 and residues 43-51 of SEQ ID NO:16, respectively). The human Bcl-2 protein is a mutant form isolated from a human lymphoma and contains a Phe (instead of Ile) residue at position 48 (Seto et al. 1988, Hockenbery et al., 1990) and two other mutations (Seto et al., 1988). Identical amino acids are indicated by solid lines, similar amino acids by colons and distantly related amino acids by single dots.

Figures 2A, 2B and 2C depict sequence homologies. Figure 2A. Homology between Nip1 (amino acids 43-100 of SEQ ID NO:21) and the catalytic domain of rat calmodulin (CaM)-dependent phosphodiesterase (PDE) (SEQ ID NO:34) (Repaske et al., 1992). Similar homologies are also observed with mouse and cattle PDE's. Figure 2B. Putative Ca^{2+} -binding motif of Nip2 (amino acids 79-90 of SEQ ID NO:23). O indicates an oxygen-containing residue, * indicates non-conserved residues and underlined residues are those that conform to the consensus. Figure 2C. Homology between Nip2 (amino acids 168-299 of SEQ ID NO:23) (lower case letters) and human GTPase activating protein, RhoGAP (SEQ ID NO:35), (Barford et al., 1993; Lancaster et al., 1994).

Isolated, in the context of the instant invention, indicates that some intervention occurs which increases the level of purity of a molecule over that found in nature.

Derivatives in the context of the instant invention is contemplated to include any modifications to the molecules of interest, including truncation, fusion, complexing to carriers and the like which brings about a physical change in the parent molecule but does not alter substantially the biologic function thereof in relationship to the parent molecule. Biologic function may be enhanced or may be lowered so long as a desirable and tolerable level is maintained. A lowered activity is palatable when a subsidiary characteristic is enhanced, for example, solubility in an aqueous medium. Alternatively, a change in the sequence that gives a mutant may yield activity that is opposite of that of the parent molecule.

It should be noted that sequence identity whether at the peptide or nucleic acid level, while preferred under certain circumstances, is not a sine qua non condition in the instant invention. A key determinant, thus, is not the absolute sequence per se but the function ascribed to the molecule or to a product of the molecule. Hence, functional equivalence is the guiding directive as to the molecules of the instant invention. Accordingly, by way of example, any one or all of the amino acids in the motifs described herein can be substituted so long as binding activity with the target of the parent sequence is retained. As noted hereinabove, as to the level of binding, that degree is mandated by the design, choice and end use of the motif derivative, and the artisan can configure and determine same without undue experimentation practicing the methods set forth herein.

The instant active agents regulate cell survival, that is, cell survival can be enhanced or prolonged or cell survival can be curtailed or shortened.

As noted hereinabove, there are molecules which have the effect of prolonging cell survival. Examples are Bcl-2 and E1B 19K. Such proteins appear to subvert apoptosis and thereby prolong cell survival. To prolong cell survival is to generate cells that statistically survive longer than expected.

The *in vivo* genetic strategy designated 'two hybrid' cloning (Fields and Song, 1989; Chien et al., 1991) permits rapid genetic screening in yeast of molecules that associate and the method has been used to isolate from expression libraries cDNA clones that code for proteins interacting with several known proteins.

Briefly, the method relies on the double transformation of yeast hosts with plasmids that encode fusion proteins. One plasmid carries partial sequences for a reporter molecule, for example, the GAL4 DNA binding domain, at the amino terminus of the fusion protein and sequences for the known protein, to which a ligand is sought, also known as the "bait" at the carboxyl terminus. For example, the bait can be the 19K protein or Bcl-2 protein.

The second plasmid comprises sequences encoding a complementary protein for the reporter molecule, in the above case, required by the GAL4 DNA binding domain, such as the GAL4 activation domain, at the amino terminus and expressed products of individual cDNA's from a bank at the carboxyl terminus. A suitable host is used to enable the selection planned, in the scenario discussed, the host would be one wherein the expression of β -galactosidase is under the control of the GAL1 promoter.

Selection of double transformants are those that express β -galactosidase, hence would be blue colonies on an X-gal plate because the bait and protein encoded by the cDNA of the second plasmid bind and that interaction juxtaposes the two GAL4 regulatory elements required for β -galactosidase expression.

In the case where 19K or Bcl-2 is the bait, the cDNA's identified thereby, encode polypeptides that bind 19K, Bcl-2 or both. Hence, those proteins have a key role in apoptosis whether by functionally and directly regulating one or more of the observable characteristics (symptoms) of apoptosis or by affecting the survival enhancing activity of 19K or Bcl-2, possibly by binding thereto.

As is known in many biologic systems, because of the tertiary and quaternary configuration of molecules and the interactions therebetween, often small portions of a molecule can have key functions, such as a recognition function, a signalling function, a catalytic function, a binding function and the like. For example, a specific antigenic determinant may comprise as few as five to six contiguous amino acids of a polypeptide and the variability and diversity of antibodies is generated by a non-contiguous plurality of short amino acid stretches in the heavy and light chains that vary from clone to clone.

Similarly, the binding interaction of an apoptosis-regulating protein, such as 19K and bcl-2, with another apoptosis-regulating molecule, such as Nip1, Nip2, Nip3 and Bip1A, disclosed herein, is governed and mediated at least in part by certain sites of the proteins which are contiguous portions of the proteins which comprise short conserved motifs or consensus sequences of amino acids. The motifs can comprise 15 amino acids or less, often 10 amino acids or less. Two motifs are AAPAPGFFS (SEQ ID NO:1) and YRRDFAE (SEQ ID NO:2) of Bcl-2 and YKWEFEE (SEQ ID NO:3) and AAAVAFLS (SEQ ID NO:4) of 19 K. Those sequences play crucial roles in the interaction between regulating molecules. Related sequences, e.g., YbxaFxEx (SEQ ID NO:5), where b is a basic amino acid, x is any amino acid and a is an acidic amino acid, and AAhAhFhS (SEQ ID NO:6), where h is a hydrophobic amino acid, may be important for the interaction as well.

It is likely that mutation at the site of the motif can have consequences related to the normal functioning of the apoptosis regulating molecules and interaction therebetween. For example, the motif from a normal B cell clone of Bcl-2 was found to be AAPAPGIFS (SEQ ID NO:7) (Cleary, 1986). On the other hand, the motif obtained from a follicular lymphoma-derived clone of bcl-2 was found to be AAPAPGFFS (SEQ ID NO:1). Also, the bcl-2 consensus may endure some variability having a sequence YRGDFAE (SEQ ID NO:32) (Tsujimoto & Croce, 1986).

That observation demonstrates the importance of the consensus sequence in the normal state and provides a differential marker for identifying and screening abnormal cells based on the amino acid substitution.

The instant nucleic acids and polypeptides may be obtained as described herein, that is by recombinant means, or may be used to obtain homologous nucleic acids and proteins by hybridization, for example, an instant nucleic acid can be used as a probe of a gene bank to identify clones with suitable homology therewith. Also, within the confines of available technology, the nucleic acids and polypeptides may be synthesized *in vitro* using, for example, solid phase oligonucleotide and oligopeptide synthetic methods known in the art.

The interactions between the apoptosis-regulating proteins, such as 19K and Bcl-2, and the proteins of the instant invention that bind thereto may take a variety of forms. For example, the molecules may either promote or suppress apoptosis on their own. The 19K and Bcl-2 type proteins may recruit the proteins of the instant invention and promote cell survival by enhancing the activity thereof or by suppressing the activity thereof.

The availability of ready sources of apoptosis-regulating proteins enables the manipulation of cells for a desired purpose. For example, it is believed that certain malignancies arise from over-expression of an apoptosis-blocking gene, such as bcl-2. In that case, application or administration of an instant protein, or nucleic acid encoding said protein, can counteract the high levels of Bcl-2. In the converse, application or administration of a protein such as Bcl-2 will enhance the life span of a cell.

Hence, the instant proteins find utility in the growth and maintenance of cells and tissues in culture. The instant proteins can be added to the culture medium in similar fashion to those supplements now used, such as, fetal calf serum, glutamine and the like. Whether an inducing or blocking molecule is used will depend on the needs of the investigator and the cell or tissue cultured.

The instant proteins that enhance cell survival can be used to maintain valuable cells without the usual "malignant" transformation methods now used. Hence, culture medium can contain one or more of the instant proteins or cells can be transfected by an expressible nucleic acid encoding the desired protein(s). Such a transfection can be by known means, such as microinjection or by precipitation, and the vector can be one which is retained episomally or integrates into the host genome. The vector comprises known regulatory elements, including optionally a signal sequence nucleic acid fragment, to ensure proper expression, such as a promoter, enhancer, terminator and the like. The starting materials and methods are available in the art.

It is evident that the instant molecules can find utility in vivo using those administration means found suitable for oligopeptides, proteins and nucleic acids. The instant molecules may be encapsulated, for example, in a liposome or in an implantable depot to overcome some of the known administration problems which might confound adequate delivery and activity at a site. Moreover, the instant molecules may be conjugated to cell binding molecules for direct targeting to a site.

The uses of the instant molecule are contingent on the impact thereof on cell survival. The use of biologics in pharmaceutical preparations is known in the art. Hence, the instant molecules could find application in treatment and amelioration of immune disorders, abnormal states characterized by aberrant cell growth and the like.

The instant molecules of apoptosis-regulating activity find utility in diagnostic assays for the presence and expression of relevant nucleic acids, presence and expression of relevant proteins, presence and functionality of binding between the two classes of molecules and the like. Use of, for example, the oligopeptide motifs in a solid-phase micro-assay would enable identifying whether functional apoptosis-regulating molecules are present in a sample. Hence, expression and extracellular presence of apoptosis-regulating proteins in degenerative diseases, such as Alzheimer's disease and spina bifida, may be diagnostic of those disorders.

Hence, the instant motif oligopeptides can be affixed to a solid phase, such as plastic microtiter dishes, using methods obtained from immunology for the fixing of antigen or antibody to a plate and then a sample is added. Following suitable washes, the presence of and amount of bound material is assessed, for example using a labelled antibody specific for the apoptosis-regulating molecules and the amount of label is assessed. Alternatively, the assessment can be visual under a microscope and the like. Alternatively, the motif can be labelled, applied to a sample and the label present assessed, similar to known radioreceptor assays, such as those for hormones using the hormone receptor as a specific reporter.

Such an assay which turns on the functional association between an apoptosis regulating molecule can be beneficial in identifying drugs that impede or prevent the interaction of the apoptosis regulating molecules.

As disclosed herein, some of the instant proteins bear homology to known proteins with a characteristic biologic activity. Hence, presence and amount of an apoptosis-regulating molecule can be ascertained by assaying for that biologic activity. For example, if a regulating molecule has enzymatic activity, then an assay for the presence and amount of that regulating molecule may rely on the assay of that enzymatic activity.

Hence, the amount of apoptosis-regulating molecules now can be ascertained in a sample using either of the two binding molecules as a receptor for the other.

Alternatively, rather than monitoring presence of the relevant molecules by physical characterization, for example, electrophoresis, or by activity, for example, an assay of an enzymatic activity, the instant molecules can be ascertained indirectly by ligands other than one or the other, for example, a ligand such as a lectin or an antibody.

As to antibodies, such specific reagents can be made using known techniques and using the target molecule as antigen. If the target molecule is poorly immunogenic, known methods for enhancing immunogenicity, such as, use of adjuvants, use of fragments of the target molecule as antigen, conjugating the target molecule or fragments thereof to a known carrier, such as albumin or keyhole limpet hemocyanin, immunizing immune cells in vitro and the like, as known in the art can be used. Either polyclonal or monoclonal antibodies can be made. For example, the 2G9 antibody reacts with the 15 kd TIA-1 protein which is related to apoptosis (Tian et al., 1991). Thus, by obtaining and using such antibodies, presence and amount of a target molecule can be determined using any of the known immunoassay formats.

The invention now will be described by reference to the following non-limiting examples.

EXAMPLE 1

A fusion protein consisting of the yeast GAL4 DNA-binding domain (amino acids 1-147) and E1B 19 kD protein (residues 2-175) expressed from a yeast shuttle vector (pMA424-19K or pAS-19K) was used as a bait in the two hybrid screen. The DNA sequences coding for the bait proteins were generated by PCR and cloned between the unique EcoRI and BamHI sites of pMA424 and pAS1 in the case of 19 kD (or between the EcoRI and SalI sites in the case of Bcl-2).

Plasmids expressing the 19 kD bait and a human cDNA expression library designated pACT (Durfee et al., 1993) tagged with the GAL4 activation domain (Durfee et al., 1993) were used for simultaneous transformation of yeast indicator strains, GGY1::171 (Gill and Ptashne, 1987) or Y153 (Durfee et al., 1993) by the lithium acetate method of Schiestl & Giest (1989). Functional reconstitution of the GAL4 transactivation function through interaction between the 19 kD moiety of the GAL4(1-147)-19K fusion protein and the cellular protein tagged with the activation domain of GAL4 activates expression of the lacZ reporter gene in strain GGY1::171 and both the HIS3 and lacZ genes in strain Y153.

Transfected cells were plated on synthetic dropout medium (SD), Rose et al., 1990, lacking leucine and histidine (strain GGY::171) or lacking histidine, tryptophan and leucine (strain Y153) by including 12.5 to 25 mM 3-AT 3-aminotriazole, a chemical which restores histidine auxotrophy (Kishore and Shaw, 1988). After three (GGY::171) to five (Y153) days at 30°C, colonies were lifted onto nitrocellulose filters (Schleicher and Schuell, BA85) and made permeable by freezing the filters for 5-10 sec on aluminum foil floats placed over liquid nitrogen.

Filters were overlaid on Whatman filters saturated with Z buffer (Miller, 1972) containing 1mg/ml X-Gal and incubated at 30°C (Breedan and Nasmyth, 1985). Colonies which turned blue within a period of 1-6 hr were picked and patched onto fresh selective plates.

The cells then were diluted in TE (10 mM Tris, pH 8.0 and 1 mM EDTA), plated onto selective plates and well-isolated colonies which were positive in the X-Gal assay were selected. Cells from the isolated colonies were patched onto selective plates and were then grown in selective liquid SD media. After overnight growth, the plasmid DNAs were extracted from the cells using glass beads (Hoffman and Winston, 1987) and the recovered DNA was used to transform an *E. coli* leuB strain (obtained from Stanley Fields, S.U.N.Y. Stony Brook) by electroporation using a BRL Cellporator according to the specifications of the manufacturer.

Ampicillin-resistant colonies were selected and replica plated on minimal M9 plates lacking amino acids to eliminate the plasmid expressing the bait protein. Plasmid DNA (containing the LEU marker) from colonies which grew on M9 media was prepared by alkaline lysis. The interaction between the 19 kD protein and the proteins coded by the cDNA clones was further ascertained by a second round of yeast transformation and X-gal staining. The cDNA clones which were positive with pMA-19K or pAS-19K and not with pMA424 or pAS1 vectors were selected for further analysis. The interaction of the selected cDNA clones with various heterologous protein baits then was determined to further ascertain the specificity of interaction with the 19 kD bait.

About 10⁵ transformants of each strain were screened for the activation of the reporter genes and three strongly positive clones were chosen for further analysis. The clones were tested in the two hybrid screen with either the 19K bait or with the GAL4 DNA binding domain vectors, pMA424 (Ma & Ptashne, 1987) or pAS1 (Durfee et al., 1993). All three clones (22, 44 and 91) reacted positively only with the 19K bait and not with the respective vectors.

The three clones (22, 44 and 91) were found to be defective in interaction with 19K mutant baits of interest.

EXAMPLE 2

To determine the specificity of the two hybrid interaction, the three clones, 22, 44 and 91, were tested against baits expressing several heterologous proteins (Table 1). Among the various heterologous protein baits used, the adenovirus E3 11.6 kD protein is of particular interest as that protein localizes on the nuclear envelope region and has an internal hydrophobic domain like the E1B 19 kD protein (Scaria et al., 1992). All three clones were negative against all the heterologous protein baits tested, indicating that the proteins coded by the clones specifically interact with the 19 kD protein.

Table 1

Interaction of cellular apoptosis-regulating proteins with heterologous protein baits [@]				
Bait	lacZ expression (X-gal)			
	clone 22	clone 44	clone 91	
19 kD	B	B	B	B=Blue W=White
HIV-1 Rev	W	W	W	
HIV-1 Tat	W	W	W	
HIV-1 Nef	W	W	W	
HTLV-I Rex	W	W	W	
SNF1	ND	W*	W*	
E1A-Exon2	W	W	W	
h-lamin	W	W	W	
E3-11.6 kD	W	W	W	
The heterologous baits pLAM5 (human lamin) and pAS-SNF1 (yeast SNF1) have been described (Bartel et al., 1993, Durfee et al., 1993). Baits pHIV-1 Rev, pHIV-1 Tat, pHIV-1 Nef and pHTLV-1 Rex expressing the various HIV or HTLV regulating proteins were constructed as described herein and obtained from Clea D'Sa Eipper and T. Subramanian, St. Louis University Medical Center, St. Louis, MO._				

[@] Interactions with all baits except the yeast SNF1 protein were carried out in yeast strain GGY1::171. Interaction with SNF1 was carried out in yeast strain Y153.

* Colonies which appeared on -his, -trp, -leu plates after 6-8 days. Results of X-gal staining are indicated as B, blue; W, white; or ND, not done.

EXAMPLE 3

Proteins coded by the various cDNA clones were prepared by in vitro transcription and translation using the phage T7-based expression vector, pET3b (Studier et al., 1990) and a commercially available kit (Promega, Madison, WI). ³⁵S-labeled proteins coded by clones 22, 44 and 91 were incubated with protein extracts prepared from human 293 cells (Graham et al., 1977) which express abundant amounts of 19 kD protein or extracts of HeLa cells which do not express any adenovirus proteins. The interaction of the labeled proteins with the 19 kD protein then was analyzed by immunoprecipitation with an antibody specific for the 19 kD protein (Green et al., 1982). The 293 cell extract was used as a source of 19 kD protein rather than purified protein since the cell extract may be suitable to detect interaction of exogenously added proteins with 19 kD protein if the interaction occurs indirectly via other cellular proteins.

Exogenously added ³⁵S-labeled proteins coded by both clones readily were precipitated with 19K antibodies in the presence of 293 cell extracts. Under the same binding conditions, ³⁵S-labeled luciferase (control) was not precipitated. Similarly, no significant amounts of the various labeled proteins were precipitated from HeLa cell extracts.

In all cases, immunoprecipitations with normal rabbit serum also did not precipitate any detectable levels of the proteins.

The results indicate that the proteins coded by clones 22, 44 and 91, (hereafter referred to as 19K-interacting protein (Nip) 1, Nip2 and Nip3, respectively) specifically interact with the 19 kD protein either directly or indirectly and substantiate the results obtained by the two hybrid screens.

EXAMPLE 4

To confirm the interaction of the Nip proteins with the 19 kD protein in vivo, BSC40 were transfected with plasmid vectors expressing the 19 kD or various Nip proteins under the transcriptional control of the T7 promoter in a mamma-

lian expression vector, pTM1 (Moss et al., 1990). The cells were infected with the recombinant vaccinia virus vTF7-3 expressing the T7 RNA polymerase gene (Fuerst et al., 1986) to induce the expression of proteins from the various pTM1 plasmids. To facilitate the analysis of protein interactions, the Nip proteins were tagged with an epitope corresponding to a 9 amino acid region of the haemagglutinin (HA) protein of influenza virus (Field et al., 1988). The pTM1 vector expressing only the HA epitope was used as a control.

Cells were labeled *in vivo* with a ^{35}S -methionine and ^{35}S -cysteine mixture, lysed and the lysates divided and subjected to immunoprecipitation analysis using either a monoclonal HA antibody 12CA5 (Boehringer-Mannheim, Indianapolis, IN) or a 19 kD antipeptide antibody (Green et al., 1982). The precipitated proteins were analyzed by SDS-PAGE and autoradiography to determine whether comparable levels of the 19 kD protein were present in each sample. The HA immunoprecipitates were separated by SDS-PAGE, blotted onto nitrocellulose and probed with the 19 kD antibody to detect the presence of coprecipitating 19 kD protein. A horseradish peroxidase-chemiluminescent detection system (ECL) (Amersham, Arlington Heights, IL) was used to visualize bound antibodies.

The 19 kD protein was not detected in HA immunoprecipitates from cells transfected with the pTM1-HA vector and pTM1-19kD, but clearly was seen coprecipitating with HA-tagged Nip1, Nip2 and Nip3.

Cells also were cotransfected with plasmids expressing each of the Nip proteins and either the 19 kD or the vector plasmid. Cell lysates were immunoprecipitated with the 19 kD antibody, blotted and probed with anti-HA antibody. That experimentation yielded comparable results for Nip1 and Nip3 (Nip2 is not transferred to nitrocellulose under standard blotting conditions) and provides additional support for the specificity of the interactions.

The results indicate that the 19 kD protein interacts specifically with each of the Nip proteins in an *in vivo* immunoprecipitation assay.

EXAMPLE 5

To determine the subcellular localization of the 19 kD-interacting proteins and to investigate whether the proteins colocalize with the 19 kD protein within the cell, COS7 cells (Gluzman, 1981) with plasmids expressing the protein coding sequences of the cDNA clones either alone or with a 19 kD-expressing plasmid were cultured and the transfected cells were analyzed by indirect immunofluorescence. To facilitate the immunofluorescence analysis of the 19 kD-interacting proteins, the proteins first were tagged with an epitope corresponding to a 9 amino acid region of the hemagglutinin (HA) protein of influenza virus (Field et al., 1988).

The cDNA's were cloned into the expression plasmid pCMV-HA which tags the proteins with an HA epitope. Cos 7 cells, grown on 22 mm² coverslips in 30 mm dishes, were transfected with plasmids expressing the 19 kD protein (pRc-CMV-19K) and/or each of the pCMV-HA based cDNA clones using the LipofectAMINETM reagent (Gibco-BRL) following the manufacturer's protocols. Forty eight hours post-transfection cells were fixed with 3.7% formaldehyde in PBS and permeabilized with ice-cold methanol. Cells were double stained with mouse monoclonal anti-HA (Berkeley Antibody Co., Inc.) and rabbit polyclonal anti-19 kD peptide serum (Green et al., 1982), and visualized with goat anti-rabbit rhodamine conjugate (Cappel) and goat anti-mouse fluorescein conjugate (Pierce). Cells were observed and photographed for rhodamine (19 kD) and fluorescein (HA-tagged clones) fluorescence. The localization of each cellular protein was examined in the absence of or presence of the 19 kD protein. The 19 kD protein primarily was expressed at the nuclear envelope/endoplasmic reticulum region. Nip1 (clone 22) and Nip2 (clone 44) also appear to be concentrated primarily on the nuclear envelope region in addition to other cytoplasmic structures. Nip3 (clone 91) has a different pattern of localization having a punctate pattern resembling the patterns exhibited by mitochondria (Alberts et al., 1989).

In cells coexpressing Nip1, Nip2 or Nip3 and the 19 kD protein, both the 19 kD and each of the cellular proteins colocalized primarily at the nuclear envelope region. Hence, the apoptosis-regulating cellular proteins localize identically with the 19 kD protein, which includes a marked shift in the localization pattern of Nip3.

EXAMPLE 6

The two hybrid strategy provides a rapid method for genetic analysis of *in vivo* protein-protein interaction. A series of 19K mutants (Table 2) with regard to ability to protect against cell death induced by the DNA damaging agent cisplatin and to cooperate with E1A in transformation of primary cells were used (Subramanian et al., 1993). The wild type 19K sequence is identified as SEQ ID NO:8; the 14-5 mutant as SEQ ID NO:9; the 29-0 mutant as SEQ ID NO:10; the 50-1 mutant as SEQ ID NO:11; the 75-6 mutant as SEQ ID NO:12; the 90-6 mutant as SEQ ID NO:13; the 123-4 mutant as SEQ ID NO: 14; and the 146-E mutant as SEQ ID NO:15.

In Table 2 the names of the various mutants are marked above the amino acid sequence and the amino acid changes are indicated below the sequence. The actual amino acids involved in the various mutations are indicated in boldface. Z indicates a stop codon. Δ indicates deletion. The underlined sequence is homologous to conserved domain I of bcl-2 (Williams & Smith, 1993).

Table 2. 19K and Bcl-2 Mutants

5	E1B 19K			
		14-5	29-0	50-1
	1	MEAWECLEDFSAVRNLLLEQSSNSTSWFWRFLWGSSQAKLVCR IKEDYKWEFEELLKSCGE		
		AS	AS	AS
10		75-6	90-6	
	61	LFD SLNLGHQALFQEKVIKTLD FSTPGRAAAAVAFLSFIKDKWSEETHLSGGYLLDFLAM		
		AS	Δ	
15		123-4	146-E	
	121	HLWRAPVVRHKNRLLLLSSVRPAIIPTEEQQFEARRRRRQEQSPWNPRAGLDPRE		
		AS	SZ	
20	Bcl-2 (Seto et al., 1988)			
			42-8	
	1	MAHAGRSGYDNREIVMKYIHYKLSQRGYEWDA GDVGAAPPGAAPAPGFFSSQPGHTPHPA		
			Δ	
25		80-6	106-5	
	61	ASRDPVARTSPLQTPAAPGAAAGPALSPVPPVH LTLRQAGDDFSRRYRRDFAEMSSQLH		
		Δ	Δ	
30	121	LTPFTARGCFATVVEELFRDGVNWGRIVAF FEGGVMCVESVNREMSPLVDNIALWMTEY		
	181	LNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYLGHK		
35				

40 The 19K-coding regions of the mutants were cloned in the pMA424 vector and tested for ability to interact with Nip1, Nip2 and Nip3 in the two hybrid assay. The interaction was assessed by determining the level of lacZ expression by the X-gal filter blue/white color assay as well as by a quantitative ONPG-based β-galactosidase assay (Rose et al., 1990) (see Table 3).

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50

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Table 3

Interaction of cellular apoptosis-regulating proteins with 19K mutants							
Mutant	Cell death suppression@	Interaction (Relative)		with cellular level of lacZ		proteins expression)	
		Nip1		Nip2		Nip3	
		X-gal	ONPG	X-gal	ONPG	X-gal	ONPG
wt	+	B	1	B	1	B	1
14-5	(+)	B	0.61	B	0.55	LB	0.16
29-0	+	B	0.33	B	0.32	B	0.19
50-1	-	W	<0.01	W	0.09	W	0.01
75-6	+	B	1.72	B	1.60	B	0.22
90-6	-	W	<0.01	W	0.04	W	0.01
123-4	-	W	0.05	LB	0.24	LB	0.10
146-E	+	B	0.87	B	0.98	B	0.28

The protein interaction studies were carried out in yeast strain GGY1::171. Results of X-gal staining are indicated as B, blue; W, white; or LB, light blue.

@ Results on suppression of cell death are based on Subramanian et al. (1993).

(+) Indicates positive at reduced levels.

β -galactosidase activities were determined from 3 to 4 independent colonies selected at random and grown in liquid selective SD medium (Rose et al., 1990). The β -galactosidase activity is expressed in units described by Rose et al., 1990.

All three 19 kD-interacting proteins were negative for interaction with mutants 50-1 (amino acids 50-51) (SEQ ID NO:11) and 90-6 (amino acids 90-96) (SEQ ID NO:13). Nip1 and Nip2 interacted at a reduced level with mutant 123-4 (substitutions for residues 123-124) (SEQ ID NO:14), but interacted more efficiently with the 19K mutant 75-6 (which carries a substitution for residues 75-76) (SEQ ID NO:12) than with wild-type (wt) 19K (SEQ ID NO:8).

Nip3 also exhibited a similar pattern of interaction; however, the overall level of expression of lacZ was lower. The studies identify two critical regions of the 19 kD protein marked by mutants 50-1 (SEQ ID NO:11) and 90-6 (SEQ ID NO:13) required for interaction with the cellular apoptosis-reducing proteins. In addition, sequences around residues 123-124 (mutant 123-4) (SEQ ID NO:14) also may influence the interactions.

The pattern of interaction of the three cellular proteins with the 19 kD protein is diagrammatically illustrated in Figure 1. All the 19K mutants used make stable proteins in mammalian cells (Subramanian et al., 1993) and in yeast as GAL-4(1-147)-19 kD fusion proteins. Thus, the 19K mutants 50-1 (SEQ ID NO:11) and 90-6 (SEQ ID NO:13) defective for suppression of cell death, also are defective for interaction with the cellular proteins. The interaction of the cellular proteins with mutant 123-4 (SEQ ID NO:14) which also is defective in suppression of cell death is, in general, much reduced.

EXAMPLE 7

Since Bcl-2 functionally can substitute for 19K during adenovirus replication, the 19 kD-interacting cellular proteins also were shown to interact with the Bcl-2 protein.

The two hybrid analysis using a pMA424-based bait expressing the human Bcl-2 protein (Hockenbery et al., 1990) was used. Plasmids pMA-Bcl2 and pAS-Bcl2 express residues 1-239 of Bcl2. Yeast cells (GGY1::171) were transformed either with the pMA424-19K bait or with the pMA424-Bcl-2 bait along with each of the activation domain-tagged cDNA clones. The expression of lacZ was determined by the X-gal filter assay as well as by the liquid ONPG β -galactosidase assay (Table 4).

Table 4

Interaction of 19 kD-interacting proteins with Bcl-2				
Protein	Relative level of lacZ expression@			
	19 kD		Bcl-2	
	X-gal	ONPG	X-gal	ONPG
Nip1	B	1	B	1.8
Nip2	B	1	B	0.7
Nip3	B	1	B	1.5

@ Relative interaction is based on the β -galactosidase activity expressed in cells expressing the respective tagged cDNA clones and the 19K bait. B, blue.

All three clones interacted with the Bcl-2 bait. Nip1 and Nip3 in general interacted more efficiently with the Bcl-2 bait as compared with the 19 kD bait. The interaction of Nip2 was slightly lower with Bcl-2 than with 19 kD.

Proteins coded by the three cDNA clones were prepared by in vitro transcription and translation according to protocols supplied by commercial vendors and incubated with cell extracts prepared from CHO cells or CHO cells infected with an adenovirus recombinant that overexpresses the human Bcl-2 protein (Ad-Bcl2) (obtained and available from T. Subramanian and B. Tarodi, St. Louis University Medical Center, St. Louis, Missouri). The proteins were immunoprecipitated with a hamster monoclonal antibody specific for human Bcl-2 (Hockenbery et al., 1990) and analyzed by SDS-PAGE.

All three 19 kD-interacting proteins could be precipitated from extracts prepared from cells infected with the Ad-Bcl2 virus while in contrast there was no significant amount of proteins precipitated from uninfected cells.

To further substantiate the interaction of the Nip proteins with Bcl-2, BSC40 cells infected with vTF7-3 (Fuerst et al., 1986) expressing the T7 RNA polymerase gene and cotransfected with plasmids expressing Bcl-2 and one of the HA-tagged Nip proteins were labeled, lysed and analyzed essentially as described in Example 4 for the 19 kD protein. Comparable levels of Bcl-2 protein were present in each sample as determined by immunoprecipitation using the Bcl-2 monoclonal antibody 6C8 (Hockenbery et al., 1990). Each sample was subjected to immunoprecipitation using the HA monoclonal antibody 12CA5 (Boehringer-Mannheim); the precipitated proteins were separated by SDS-PAGE, blotted and probed for the presence of Bcl-2. Bcl-2 clearly was coprecipitated with HA-Nip1, HA-Nip2 and HA-Nip3.

An alternate experiment in which the cells were cotransfected with each of the Nip proteins and either Bcl-2 or the vector plasmid and cell lysates were immunoprecipitated with antibody directed against the Bcl-2 protein and probed with anti-HA antibody, yielded comparable results for Nip1 and Nip3 (Nip2 is not transferred to nitrocellulose under standard blotting conditions) and provides additional support for the specificity of the interactions. Thus, using in vivo coimmunoprecipitation, a specific interaction between each of the Nip proteins and Bcl-2 was found. The results, together with the in vitro immunoprecipitation data, indicate that the three Nip proteins interact with Bcl-2 as well as with the 19 kD proteins.

Using bcl-2 as the bait in the two hybrid analysis, three additional regulating proteins (Bip for bcl-2 interacting protein) were identified. Two of the clones (Bip 1A, SEQ ID NOS:26-27 and Bip 13, SEQ ID NOS:30-31) also interact with the 19K bait, while clone Bip 5, SEQ ID NOS:28-29, did not. Bip 1A was tested for interaction with the 19K mutants as described in Example 5 and exhibited a similar pattern of interaction to that seen with NIP's 1, 2 and 3. Interaction was negative with mutant 90-6 (SEQ ID NO:13) and greatly diminished with mutant 50-1 (SEQ ID NO:11), as illustrated in Figure 1.

EXAMPLE 8

The observation that the various 19 kD-interacting proteins also interact with the Bcl-2 protein is significant since the primary amino acid sequence of the 19 kD protein is not significantly homologous to Bcl-2 and related proteins (reviewed by Williams and Smith, 1993). Since four cellular proteins tested (Nip1, Nip2, Nip3 and Bip1A) failed to interact with 19K mutants 50-1 (SEQ ID NO:11) and 90-6 (SEQ ID NO:13), regions of homology corresponding to the mutated regions of 19 kD protein must exist. Three regions of homology between the amino acid sequences encompassing the 19K mutants (50-1 and 90-6) and Bcl-2 were identified.

Based thereon, three different deletion mutants within the Bcl-2 (SEQ ID NO:16) coding region were constructed by oligonucleotide-directed mutagenesis using commercially available kits (Amersham) (Table 2). The mutants lack Bcl-2 (SEQ ID NO:16) residues 42 to 48 (#42-8) (SEQ ID NO:17), 80 to 86 (#80-6) (SEQ ID NO:18) and 106 to 115 (#106-5) (SEQ ID NO:19) of Bcl-2. The mutants were cloned in pMA424 and used in the two hybrid assay. Interaction was determined by the lacZ expression assays (Table 5).

Table 5

Interaction of 19 kD-interacting proteins with Bcl-2 mutants						
Mutant	Relative level of lacZ expression@					
	Nip1		Nip2		Nip3	
	X-gal	ONPG	X-gal	ONPG	X-gal	ONPG
wt	B	1.0	B	1.0	B	1.0
42-8	W	0.16	W	0.09	W	0.19
80-6	B	1.21	B	0.80	B	2.87
106-5	W	0.01	W	0.06	W	0.11

@ Relative interaction is based on the β -galactosidase activity expressed in cells expressing the respective tagged cDNA clones and the Bcl-2 baits expressing the various mutants. B, blue; W, white.

Mutants 42-8 and 106-5 were defective for interaction with the three clones tested while mutant 80-6 was not. Since the amino acid sequences of Bcl-2 deleted in mutants 42-8 and 106-5 appear to be homologous to sequences around 19K mutants 90-6 and 50-1, respectively, the 19 kD-interacting proteins recognize bipartite sequence motifs common to both the 19 kD and Bcl-2 proteins (Fig. 1).

EXAMPLE 9

The DNA sequences of the six cDNA clones were determined by dideoxy sequencing using the Sequenase kit (U.S. Biochemicals) of pAct-based plasmids (Durfee et al., 1993) or after subcloning into the pBluescript II KS(+) vector (Stratagene, San Diego, CA) using Sequenase version 2 (United States Biochemical Corp.). Sequencing first was initiated with primers complementary to sequences upstream of the cDNA cloning site in pAct or the T3 promoter of pBluescript. Subsequently, other primers were synthesized on the basis of newly determined sequences and used for sequencing both strands. The reading frame in relation to the GAL4 activation domain was established.

Since the activation domain is tagged at the 5' end of the cDNA's, a fraction of cDNA's isolated by the two hybrid system may be lacking the sequences corresponding to native 5' ends of the various mRNA's. Hence, the 5'-upstream sequences corresponding to the three isolated cDNA clones were obtained by reverse transcription of poly(A)-containing RNA prepared from human HeLa cells or from human placenta and PCR amplification (Frohman et al., 1988) using two nested primers (5'RACE) using a commercially available kit (5'AmplIFINDER, Clontech) or from cDNA clones isolated from a human B cell cDNA library (Ausubel et al., 1992).

Downstream sequences were obtained by 3'RACE (described hereinbelow) using a commercially available kit (GibcoBRL). The Bluescript-based cDNA clones were prepared after infection with the helper phage and sequenced using appropriate primers. The DNA fragments obtained by RACE were cloned and sequenced.

The RACE analysis provided additional DNA sequences corresponding to three codons including an ATG codon for clone 22 (Nip1) while extensive analysis did not provide additional protein coding sequences corresponding to cDNA clones 44 (Nip2) and 91 (Nip3). The coding region of clone 44 at the 3' end (30 amino acids) was obtained by 3' RACE analysis.

For Bip5, 139 bp of 5' sequences were obtained as follows. The two hybrid clone contained nucleotides 109 to 1542. Comparison of the Bip5 sequence with a human fetal brain cDNA clone revealed substantial sequence identity and overlap (clone T08302, EST 06193, Adams et al., 1993) between the two clones. Clone T08302 contains a 366 bp fragment and includes an open reading frame beginning at the ATG of the clone. T08302 was ligated to the 5' end of the Bip5 clone following PCR amplification.

EXAMPLE 10

The amino acid sequences of Nip1 (SEQ ID NO:21), Nip2 (SEQ ID NO:23), Nip3 (SEQ ID NO:25), Bip1A (SEQ ID NO:27), Bip5 (SEQ ID NO:29) and Bip13 (SEQ ID NO:31) based on DNA sequences are presented in Table 6. Putative transmembrane domains of Nip1 and Nip3 are underlined.

The amino acid sequences were analyzed to determine if any similarity to other sequences existed in various known and available data banks (GenBank, PIR and SwissProt National Center for Biotechnology Information (NCBI) using the FASTA, TFASTA programs (Pearson & Lipman 1988) available in the University of Wisconsin Genetic Computer group (UWGCG package) and BLAST (NCBI) (Alschul et al., 1990) algorithms. The sequences also were analyzed by the PROSITE (UWGCG Software package) program to identify functional sequence motifs.

Nip1 (SEQ ID NO:21) is a 228 amino acid protein and contains a putative membrane-spanning hydrophobic domain. The presence of the membrane-spanning domain enables the protein to form stable associations with cellular membranes and accounts for the observed localization of the protein to the nuclear envelope/endoplasmic reticulum region of the cell.

Sequence comparison of Nip1 (SEQ ID NO:21) indicated that the protein is not significantly homologous to other known proteins. However, a 59 to 83 amino acid region of Nip1 has homology (29 to 36 per cent identity and 55 to 60 per cent similarity) to a conserved region (Figure 2A) within the catalytic domain of three mammalian (rat, mouse and cow) calmodulin-dependent 3'-5'-cyclic nucleotide phosphodiesterases (PDE) (SEQ ID NO:34) (Bentley et al., 1992; Polli et al., 1992; Repaske et al., 1992).

Because Nip1 is likely to possess an enzymatic activity, Nip1 can be used as a diagnostic tool to ascertain the state of the cell. Hence, excess of reduced Nip1 phosphodiesterase activity can be a means for monitoring the metabolic state of a cell, tissue or organ.

Nip2 (SEQ ID NO:23) is a 314 amino acid protein. Sequence comparison revealed that a 126 amino acid region of Nip2 shares significant homology (47 per cent identity and 66 per cent similarity; Figure 2C) to the human GTPase activating protein RhoGAP (SEQ ID NO:35) (Barfod et al., 1993; Lancaster et al., 1994). The homology between Nip2 and RhoGAP does not extend to the functional domain of RhoGAP and is located in an upstream region which has been postulated to be removed by proteolysis (Barfod et al., 1993).

A scrutiny of the Nip2 sequence also revealed the presence of a putative Ca^{++} -binding motif (amino acids 79-90 of SEQ ID NO: 23) (Figure 2B).

Even though Nip2 does not contain a membrane-spanning hydrophobic domain, indirect immunofluorescence analysis indicates that it is associated with cytoplasmic structures.

Nip3 (SEQ ID NO:25) is a 194 amino acid protein and contains a presumptive membrane-spanning hydrophobic domain. Nip3 also appears to be a novel protein. However, the cDNA sequence is highly homologous to a rat cDNA clone which encodes the rat brain calbindin-D protein (Hunziker and Schrickel, 1988). A smaller cDNA clone isolated from human fetal brain (Adams et al., 1992) is identical to sequences within the Nip3 coding region. cDNA clone 91 (Nip3) and the fetal brain cDNA do not contain the coding sequences for calbindin. Similarly, two other cDNA clones containing Nip3 sequences isolated from a human B cell cDNA library do not contain the calbindin coding sequences. An extensive search for additional sequences in DNA amplified by 5'RACE of human placental RNA with primers specific for clone 91 did not yield additional 5' sequences corresponding to calbindin coding sequences.

Thus, Nip3 is coded by a unique mRNA in human cells. That notion is in agreement with the observation that rat calbindin cDNA hybridizes to multiple mRNA species from human membrane (Iacopino and Christakos, 1990).

All three cellular proteins contain sequence motifs designated PEST (enriched in proline, glutamic acid, serine and threonine) (SEQ ID NO:33) sequences (Rogers et al., 1986) suggesting that the proteins may be degraded rapidly and expressed in a stage-specific manner (Rogers et al., 1986).

Bip1A (SEQ ID NO:27) is a 160 amino acid protein.

Bip5 (SEQ ID NO:29) is a 259 amino acid protein and does not exhibit significant homology to other known proteins.

On sequencing, it was determined that clone Bip13 (SEQ ID NO:31) bears a high degree of homology with CD22 (Wilson et al., 1991; Stamenkovic and Seed, 1990). CD22 is known to increase intracellular calcium and may be a B cell activator, however, the role of CD22 in apoptosis heretofore was unknown.

Table 6. Amino Acid and Nucleic Acid Sequences

5

A. Nip1

10

AGTCCCCAACATGGCGGCTCCCCAAGACGTCCACGTCCGGATCTGTAACCAAGAGATTGT

CAAATTTGACCTGGAGGTGAAGGCGCTTATTCAGGATATCCGTGATTGTTTCAGGACCCTT

K F D L E V K A L I Q D I R D C S G P L

AAGTGCTCTTACTGAACTGAATACTAAAGTAAAAGAGAAATTTCAACAGTTGCGTCACAG

15

S A L T E L N T K V K E K F Q Q L R H R

AATACAGGACCTGGAGCAGTTGGCTAAAGAGCAAGACAAAGAATCAGAGAAACAACTTCT

I Q D L E Q L A K E Q D K E S E K Q L L

ACTCCAGGAAGTGGAGAATCACAAAAGCAGATGCTCAGCAATCAGGCCTCATGGAGGAA

L Q E V E N H K K Q M L S N Q A S W R K

20

AGCTAATCTCACCTGCAAAATTGCAATCGACAATCTAGAGAAAGCAGAACTTCTTCAGGG

A N L T C K I A I D N L E K A E L L Q G

AGGAGATCTCTTAAGGCAAAGGAAAACCACCAAAGAGAGCCTGGCCCAGACATCCAGTAC

G D L L R Q R K T T K E S L A Q T S S T

CATCACTGAGAGCCTCATGGGGATCAGCAGGATGATGGCCCAGCAGGTCCAGCAGAGCGA

25

I T E S L M G I S R M M A Q Q V Q Q S E

GGAGGCCATGCAGTCTCTAGTCACTTCTTCACGAACGATCCTGGATGCAAATGAAGAATT

E A M Q S L V T S S R T I L D A N E E F

TAAGTCCATGTCGGGCACCATCCAGCTGGGCCGGAAGCTTATCACAAAATACAATCGCCG

K S M S G T I Q L G R K L I T K Y N R R

30

GGAGCTGACGGACAAGCTTCTCATCTTCCTTGCGCTACGCCTGTTTCTTGCTACGGTCCT

35

40

45

50

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E L T D K L L I F L A L R L F L A T V L
 CTATATTGTGAAAAAGCGGCTCTTTCCATTTTTGTGAGATCCCAAAGGTGCCAGTTCTGG
 Y I V K K R L F P F L
 5 CCCTTTTCAGCTCCTGTTTCAGGATCTGTCCTGGTTCCTGAGCTCTAGGCTGCTAAGCTGA
 GCCACACACCCCTCCGTTTTGCACCAGTTGCCTGCAGGTTGGATGGAACACAGTGCCCCA
 CTTTTCTGCAAGTAGCTGGCTTGTAAGGGTGAACAGAGCCATGGGAGGAAGGTCTGGCA
 TTGGGATGCCGCCCTGGGGACATACGAACCGCCTCCTTCCACCATTGTGCACTATGGGAG
 GCCGCTGCTGCGTGGAGCACTTAAAGTCCAGCCTCCAGGACCGGATGCCCCCTCCTGTCTC
 10 CCGCTCCCATCGTGCCCTTAAATGCCAGATCTGGTGGAGGGAAGAGAGAAGAGGTAGGAA
 GAAAGGTGATGAAAACCTCTG

B. Nip2

15 CTGCGGCCGCGGGGATTGGGCCGCGGTCTCCACCGCCGACCGAG
 GGGAGCGGCGTCCGCTCGGCCCTGCTTTTTGCGACCTGCCGTGAGCCCCAGTCGCCGGC
 CTGGAGGGGCGAAGAGGACGAGGGGCGACGAAGGCCCAAGGCTTCTCCGGGGACATTGG
 CTCCCTGGATTATCAAGCAGTTTGTAGTTGACATTGAATCCAGGCTGAGGATGGAAGGTG
 20 M E G
 TGGAACTTAAAGAAGAATGGCAAGATGAAGATTTTCCGATACCTTTACCAGAAGATGATA
 V E L K E E W Q D E D F P I P L P E D D
 GTATTGAAGCAGATATACTAGCTATAACTGGACCAGAGGACCAGCCTGGCTCACTAGAAG
 S I E A D I L A I T G P E D Q P G S L E
 25 TTAATGGAAATAAAGTGAGAAAGAACTAATGGCTCCAGACATTAGCCTGACACTGGATC
 V N G N K V R K L M A P D I S L T L D
 CTAGTGATGGCTCTGTATTGTCAGATGATTGGATGAAAGTGGGGAGATTGACTTAGATG
 P S D G S V L S D D L D E S G E I D L D
 GCTTAGACACACCGTCAGAGAATAGTAATGAGTTTGAGTGGGAAGATGATCTTCCAAAC
 30 G L D T P S E N S N E F E W E D D L P K
 CCAAGACTACTGAAGTAATTAGGAAAGGCTCAATTACTGAATACACAGCAGCAGAGGAAA
 P K T T E V I R K G S I T E Y T A A E E
 AAGAAGATGGACGACGCTGGCGTATGTTTCCAGGATTGGAGAACAGGACCAGGGTTGATA
 K E D G R R W R M F R I G E Q D H R V D
 35 TGAAGGCAATTGAACCTATAAAAAAGTTATCAGCCATGGGGGATATTATGGGGATGGAT
 M K A I E P Y K K V I S H G G Y Y G D G
 TAAATGCCATTGTTGTATTGCTGTCTGTTTCATGCCTGAAAGTAGTCAGCCTAACTATA
 L N A I V V F A V C F M P E S S Q P N Y
 GATACCTGATGGACAATCTTTTTAAATATGTTATTGGCACTTTGGAGCTATTAGTAGCAG
 40 R Y L M D N L F K Y V I G T L E L L V A
 AAAACTACATGATAGTTTATTTAAATGGTGCACAACCTCGAAGAAAAATGCCCAGTCTGG
 E N Y M I V Y L N G A T T R R K M P S L
 GATGGCTCAGGAAATGTTATCAGCAAATGATAGAAGGTTACGGAAAAATCTAAATCCC
 G W L R K C Y Q Q I D R R L R K N L K S
 45 TAATCATTGTACATCCTTCTTGGTTTATCAGAACACTTCTGGCTGTTACAAGACCATTTA
 L I I V H P S W F I R T L L A V T R P F
 TTAGCTCGAAATTCAGCCAAAAAATTAGATACGTGTTTAAATTGGCAGAACTAGCAGAAC
 I S S K F S Q K I R Y V F N L A E L A E
 TTGTCCCATGGAATACGTTGGCATAACAGAATGCATAAAACAAGTTGATCAAGAAGCTTA
 50 L V P M E Y V G I P E C I K Q V D Q E L
 ATGGAACAAGATGAACCGAAAAATGAACAGTAAGTTTGGCATCTAGTCCAAACAAGAC
 N G K Q D E P K N E Q
 TGAAGAATGTGCTGATGGAGCAGTGCTGTTTCTGCATTCATAATGCATTTATTGGCCAT

55

ATTTTATGTAACCTGTTACAAAATAGACTTGACTTTTTCATAATGGACTTTTGTATTATACA
AGGGACTGTTCACTGCTGTACTGGTTTGCAAATTTCTGAATTTAGCTCTTTATGCTAACTGT
ATTATTATCATTTTATAT

5
C. Nip3

10 AAAGAGATCTGGAATTCGGATCCTCGAGGCCACGAAGGCCACCGCCCGCAGCTGAAGCAC
ATCCGCAGCCCGGCGCGACTCCGATCGCCGCAGTTGCCCTCTGGCGCCATGTCCGAGAAC
M S E N
GGAGCGCCCGGATGCAGGAGGAGAGCCTGCAGGGCTCCTGGGTAGAACTGCACTTCAGC
G A P G M Q E E S L Q G S W V E L H F S
AATAATGGGAACGGGGGCGAGCTTCCAGCCTCGGTTTCTATTATAATGGAGACATGGAA
15 N N G N G G S V P A S V S I Y N G D M E
AAAATACTGCTGGACGCACAGCATGAGTCTGGACGGAGTAGCTCCAAGAGCTCTCACTGT
K I L L D A Q H E S G R S S S K S S H C
GACAGCCACCTCGCTCGCAGACACCACAAGATACCAACAGGGCTTCTGAAACAGATACC
D S P P R S Q T P Q D T N R A S E T D T
CATAGCATTGGAGAGAAAAACAGCTCACAGTCTGAGGAAGATGATATTGAAAGAAGGAAA
20 H S I G E K N S S Q S E E D D I E R R K
GAAGTTGAAAGCATCTTGAAGAAAACTCAGATTGGATATGGGATTGGTCAAGTCGGCCG
E V E S I L K K N S D W I W D W S S R P
GAAAATATTCCCCCAAGGAGTTCTCTTTAAACACCCGAAGCGCACGGCCACCCTCAGC
E N I P P K E F L F K H P K R T A T L S
25 ATGAGGAACACGAGCGTCATGAAGAAAGGGGCATATTCTCTGCAGAATTTCTGAAAGTT
M R N T S V M K K G G I F S A E F L K V
TTCCTTCCATCTCTGCTGCTCTCTCATTTGCTGGCCATCGGATTGGGGATCTATATTGGA
F L P S L L L S H L L A I G L G I Y I G
AGGCGTCTGACAACCTCCACCAGCACCTTTTGATGAAGAACTGGAGTCTGACTTGTTTCG
30 R R L T T S T S T F
TTAGTGGAATTACTTCTGAGCTTGCAACATAGCTCACTGAAGAGCTGTTAGATCCTGGGCC
TTCGTGGCTCGAGAGACTAGAATCGCAGATACGAAAACCCCGCAGC

35 D. Bipla

CAGCATCGCCGCCCGCCAGAGGAGAAATGTCTGAAGTA
M S E V
AGACCCCTCTCCAGAGACATCTTGATGGAGACCCCTCCTGTATGAGCAGCTCCTGGAACCC
40 R P L S R D I L M E T L L Y E Q L L E P
CCGACCATGGAGGTTCTTGGCATGACTGACTCTGAAGAGGACCTGGACCCTATGGAGGAC
P T M E V L G M T D S E E D L D P M E D
TTCGATTCTTTGGAATGCATGGAGGGCAGTGACGCATTGGCCCTGCGGCTGGCCTGCATC
F D S L E C M E G S D A L A L R L A C I
45 GGGGACGAGATGGACGTGAGCCTCAGGGCCCCGCGCCTGGCCCAGCTCTCCGAGGTGGCC
G D E M D V S L R A P R L A Q L S E V A
ATGCACAGCCTGGGTCTGGCTTTTCATCTACGACCAGACTGAGGACATCAGGGATGTTCTT
M H S L G L A F I Y D Q T E D I R D V L
AGAAGTTTCATGGACGGTTTCAACACACTTAAGGAGAACATAATGAGGTTCTGGAGATCC
50 R S F M D G F T T L K E N I M R F W R S
CCGAACCCCGGGTCTGGGTGCTGCTGCGAACAGGTGCTGCTGGCGCTGCTGCTGCTGCT
P N P G S W V S C E Q V L L L A L L L
GCGCTGCTGCTGCGCTGCTCAGCGGGGCTGCACCTGCTGCTCAAGTGAGGCCCCGGC

A L L L P L L S G G L H L L L K
 GGCTCAGGGCGTGGCTGGCCCCACCCCCATGACCACTGCCCTGGAGGTGGCGGCCTGCTGCT
 GTTATCTTTTAACTGTTTTCTCATGATGCCTTTTATATTTAAACCCCGAGATAGTG
 5 CTGGAACACTGCTGAGGTTTTTATACTCAGGTTTTTGTTTTTTTTTTATTCCAGTTTTTCG
 TTTTTTCTAAAAGATGAATTCCTATGGCTCTGCAATTGTCAACGGTTAACTGTGGCCTGT
 GCCCAGGAAGAGCCATTCACTCCTGCCCCTGCCACACGGCAGGTAGCAGGGGGAGTGCT
 GGTCACACCCCTGTGTGATATGTGATGCCCTCGGCAAAGAATCTACTGGAATAGATTCCG
 10 AGGAGCAGGAGTGCTCAATAAAATGTTGGTTTCCAGCAAAAAAAAAAAAAAGGCCTTCGT
 GGCCTCGAG

E. Bip5

ATG GAC GCC TGG GTC CGC TTC AGT GCT CAG AGC CAA GCC CGG
 15 M D A W V R F S A Q S Q A R
 GAG CGG CTG TGT AGG GCC GCC CAG TAT GCT TGC TCT CTT CTT GGC
 E R L C R A A Q Y A C S L L G
 CAT GCG CTG CAG AGG CAT GGA GCC AGT CCT GAG TTA CAG AAA CAG
 H A L Q R H G A S P E L Q K Q
 20 ATT CGA CAA CTG GAG AGC CAC CTG AGC CTT GGA AGA AAG CTT CTA
 I R Q L E S H L S L G R K L L
 CGC CTG GGT AAC TCA GCA GAT GCC CTT GAG TCA GCC AAA AGA GCT
 R L G N S A D A L E S A K R A
 GTT CAC CTA TCA GAT GTT GTC CTG AGA TTC TGC ATC ACT GTT AGT
 V H L S D V V L R F C I T V S
 25 CAC CTC AAT CGA GCC TTG TAC TTC GCC TGT CAC AAT GTC CTG TGG
 H L N R A L Y F A C H N V L W
 GCT GGA AAG TCT GGA CTG GCT CCC CGT GTG GAT CAG GAG AAG TGG
 A G K S G L A P R V D Q E K W
 GCC CAG CGT TCA TTC AGG TAC TAT TTG TTT TCC CTC ATC ATG AAT
 30 A Q R S F R Y Y L F S L I M N
 TTG AGC CGT GAT GCT TAT GAG ATT CGC CTA CTG ATG GAG CAA GAG
 L S R D A Y E I R L L M E Q E
 TCT TCT GCT TGT AGC CGG CGA CTG AAA GGT TCT GGA GGA GGA GTC
 S S A C S R R L K G S G G G V
 35 CCA GGA GGA AGT GAA ACT GGG GGA CTT GGG GGA CCA GGG ACT CCA
 P G G S E T G G L G G P G T P
 GGA GGA GGT CTG CCC CAA CTG GCT CTG AAA CTT CGG CTG CAA GTC
 G G G L P Q L A L K L R L Q V
 CTG CTC CTG GCT CGA GTC CTT AGA GGT CAT CCC CCA CTT CTG CTA
 40 L L L A R V L R G H P P L L L
 GAC GTG GTC AGA AAT GCC TGT GAT CTC TTC ATT CCT CTG GAC AAA
 D V V R N A C D L F I P L D K
 CTA GCG CTC TGG CGC TGT GGC CCT GGG ATT GTG GGG CTT TGT GGC
 L A L W R C G P G I V G L C G
 45 CTC GTG TCC TCC ATC CTG TCT ATT CTC ACC CTA ATC TAT CCC TGG
 L V S S I L S I L T L I Y P W
 CTA CGA CTC AAG CCC TGA CTT CCG GTA CAG GAT AAG GAG GGG ACC
 L R L K P
 TGA ATT GGT GAG ATG GAA TCT TAG ATC GTC CCC ATG TGC CAG CCT
 50 CAT TCG AAT TCT ACT CTT TGG TTA AAG TTA GAA ATT CAG AGA TTT
 AGG GGT GGA GGA GGA AGA GCT TTG GGG AAG ATG AGG TAA GGA AAG
 ATG ACT CGT GAA GTT AAT AGG ATG TCT CTA ATT TCT AGA

55

F. Bip13

5 AGTCAAGTCGAGTTTCTTTGCATGTCACTGGCCAATCCTCTT
 S Q V E F L C M S L A N P L
 CCAACAAATTACACGTGGTACCACAATGGGAAAGAAATGCAGGGAAGGACAGAGGAGAAA
 P T N Y T W Y H N G K E M Q G R T E E K
 GTCCACATCCCAAAGATCCTCCCCTGGCACGCTGGGACTTATTCTGTGTGGCAGAAAAC
 V H I P K I L P W H A G T Y S C V A E N
 10 ATTCTTGGTACTGGACAGAGGGGCGGGAGCTGAGCTGGATGTCCAGTATCCTCCCAAG
 I L G T G Q R G P G A E L D V Q Y P P K
 AAGGTGACCACAGTGATTCAAACCCCATGCCGATTGAGAAGGAGACACAGTGACCCTT
 K V T T V I Q N P M P I R E G D T V T L
 TCCTGTAACTACAATTCCAGTAACCCAGTGTTACCCGGTATGAATGGAAACCCCATGGC
 15 S C N Y N S S N P S V T R Y E W K P H G
 GCCTGGGAGGAGCCATCGCTTGGGGTGCTGAAGATCCAAAACGTTGGCTGGGACAACACA
 A W E E P S L G V L K I Q N V G W D N T
 ACCATCGCCTGCGCACGTTGTAATAGTTGGTGCTCGTGGGCCTCCCCTGTGCGCCTGAAT
 T I A C A R C N S W C S W A S P V A L N
 20 GTCCAGTATGCCCCCGAGACGTGAGGGTCCGGAATAAAGCCCCCTTCCGAGATTCAC
 V Q Y A P R D V R V R K I K P L S E I H
 TCTGGAAACTCGGTGAGCCTCCAATGTGACTTCTCAAGCAGCCACCCCAAAGAAGTCCAG
 S G N S V S L Q C D F S S S H P K E V Q
 TTCTTTCTGGGAGAAAAATGGCAGGCTTCTGGGGAAAGAAAGCCAGCTGAATTTTGACTCC
 25 F F W E K N G R L L G K E S Q L N F D S
 ATCTCCCCAGAAGATGCTGGGAGTTACAGCTGCTGGGTGAACAACTCCATAGGACAGACA
 I S P E D A G S Y S C W V N N S I G Q T
 GCGTCCAAGGCCTGGACACTTGAAGTGCTGTATGCACCCAGGAGGCTGCGTGTGTCCATG
 A S K A W T L E V L Y A P R R L R V S M
 30 AGCCCGGGGGACCAAGTGTGAGGGGAAGAGTGCAACCCTGACCTGTGAGAGTGACGCC
 S P G D Q V M E G K S A T L T C E S D A
 AACCTCCCCTCTCCCACTACACCTGGTTTGACTGGAATAACCAAAGCCTCCCCACCAC
 N P P V S H Y T W F D W N N Q S L P H H
 AGCCAGAAGCTGAGATTGGAGCCGGTGAAGGTCAGCACTCGGGTGCCTACTGGTGCCAG
 35 S Q K L R L E P V K V Q H S G A Y W C Q
 GGGACCAACAGTGTGGGCAAGGGCCGTTGCGCTCTCAGCACCCCTTACTGTCTACTATAGC
 G T N S V G K G R S P L S T L T V Y Y S
 CCGGAGACCATCGGCAGGCGAGTGGCTGTGGGACTCGGGTCTGCTCGCCATCCTCATC
 P E T I G R R V A V G L G S C L A I L I
 40 CTGGCAATCTGTGGGCTCAAGCTCCAGCGACGTTGGAAGAGGACACAGAGCCAGCAGGGG
 L A I C G L K L Q R R W K R T Q S Q Q G
 CTTCAGGAGAATTCCAGCGGCCAGAGCTTCTTTGTGAGGAATAAAAAGGTTAGAAGGGCC
 L Q E N S S G Q S F F V R N K K V R R A
 CCCCTCTCTGAAGGCCCCCACTCCCTGGGATGCTACAATCCAATGATGGAAGATGGCATT
 45 P L S E G P H S L G C Y N P M M E D G I
 AGCTACACCACCTGCGCTTCCCGAGATGAACATACCACGAACTGGAGATGCAGAGTCC
 S Y T T L R F P E M N I P R T G D A E S
 TCAGAGATGCAGAGACCTCCCCGACCTGCGATGACACGGTCACTTATTCAGCATTGCAC
 S E M Q R P P R T C D D T V T Y S A L H
 50 AAGCGCAAGTGGGCGACTATGAGAACGTCATTCCAGATTTTCCAGAAGATGAGGGGATT
 K R Q V G D Y E N V I P D F P E D E G I

55

CATTACTCAGAGCTGATCCAGTTTGGGGTCGGGGAGCGGCCTCAGGCACAAGAAAATGTG
 H Y S E L I Q F G V G E R P Q A Q E N V
 GACTATGTGATCCTCAAACATTGACACTGGATGGGCTGCAGCAGAGGCACTGGGGGCAGC
 5 D Y V I L K H
 GGGGGCCAGGGAAGTCCCCGAGTTTCCCCAGACACCGCCACATGGCTTCCTCCTGCGTGC
 ATGTGCGCACACACACACACACGACACACACACACACTCACTGCGGAGAACCT
 TGTGCTGGCTCAGAGCCAGTCTTTTTGGTGAGGGTAACCCCAAACCTCCAAAACCTCTG
 CCCCTGTTCTCTTCCACTCTCCTTGCTACCCAGAAATCATCTAAATACCTGCCCTGACAT
 10 GCACACCTCCCCTGCCCCACCAGCCCACTGGCCATCTCCACCCGGAGCTGCTGTGTCTCT
 TGGATCTGCTCGTCATTTCCTTCCCTTCTCCATCTCTCTGGCCCTCTACCCCTGATCTG
 ACATCCCCACTCACGAATATTATGCCAGTTTCTGCCTCTGAGGGAAAGCCCAGAAAAGG
 ACAGAAACGAAGTAGAAAGGGGGCCAGTCTTGGCCTGGCTTCTCCTTTGGAAGTGAGGCA
 TTGCACGGGGAGACGTACGTATCAGCGGCCCTTGACTCTGGGGACTCCGGGTTTGAGAT
 15 GGACACACTGGTGTGGATTAACCTGCCAGGGAGACAGAGCTCACAATAAAAATGGCTCAG
 ATGCCACTTCAAAGAAAAAAAAAAAA

20

EXAMPLE 11

25 The cellular apoptosis-regulating proteins also interact with the BHRF-1 protein of Epstein-Barr virus. BHRF-1 (Baer et al., 1984; Pearson et al., 1987) shares significant homology with the Bcl-2 protein (Cleary et al., 1986; Williams and Smith, 1993). The BHRF-1 protein can protect against cell death induced by certain apoptosis-inducing stimuli such as serum depletion and the DNA damaging agents (Henderson et al., 1993). Sequences homologous to the 19 kD motifs are present in the BHRF-1 protein. The two domains of the 19 kD and Bcl-2 proteins required for interaction

30 with the cellular proteins are absent in Bax, a homolog of Bcl-2 (Oltvai et al., 1993). The absence of the two domains in Bax, which has a cell death promoting activity, supports the observation that the two domains are important for mediating cell survival by the 19 kD and Bcl-2 proteins.
 The 19 kD protein of Ad2 and Ad5 contains a region (residues 60-69) (see Table 1) homologous to a conserved domain (termed domain I) present in various Bcl-2-related proteins, including Bax (Williams and Smith, 1993; Oltvai et al., 1993). Nip1, Nip2 and Nip3 do not interact with human Bax, which contains domain I, in the yeast two hybrid assay

35 suggesting that the conserved domain I may not be essential for interaction of Nip1, Nip2 and Nip3. However, Bcl-2 can suppress cell death promoted by Bax, possibly by forming Bax-Bcl-2 heterodimers (Oltvai et al., 1993).
 In the nematode *C. elegans*, apoptotic cell death is inhibited by a survival promoting gene designated *ced-9* (Hengartner et al., 1992). The *ced-9* gene antagonizes the activity of two nematode cell death-inducing genes, *ced-3* and *ced-4*, which are activated during programmed cell death (Yuan and Horvitz, 1990). Bcl-2 can substitute functionally for *ced-9* in *C. elegans* (Vaux et al., 1991).

40 The mammalian IL-1 β -converting enzyme (ICE), a homolog of *ced-3* (Yuan et al., 1993; Miura et al., 1993), induces cell death in mammalian cells. The activity of ICE can be suppressed by Bcl-2 (Miura et al., 1993) although it is not known whether there is any physical interaction between ICE and Bcl-2.

45

EXAMPLE 12

The homology between Nip2 and Rho GTPase-activating protein (RhoGAP) raises the possibility that the signal transduction pathway may play a key role in counteracting the cell death inducing stimuli. In this context, it has recently

50 been reported that the Bcl-2 protein associates with R-ras (Fernandez-Sarabia & Bischoff, 1993), a member of Ras superfamily. Nip2 may modulate the activity of RhoGAP through alternate mechanisms such a formation of RhoGAP-Nip2 heterodimers. Because the homology between Nip2 and RhoGAP is located upstream of the N-terminus of active RhoGAP (Garrett et al., 1991), Nip2 might affect the activity of RhoGAP by interfering with the processing of RhoGAP.
 Nip2 has a putative Ca²⁺-binding motif. Since intracellular Ca²⁺ appears to be an important mediator of apoptotic

55 cell death, it is possible that the activity of Nip2 may be modulated by Ca²⁺. Hence, interactions between the 19 Kd protein and Nip2 could remove the influence thereof on RhoGAP activity, thus affecting p21^{ras} and potentially other members of the ras superfamily.

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All references cited herein are incorporated herein by reference in their entirety.

- 40 As will be evident to the artisan, various modifications and changes can be made without departing from the spirit and scope of the instant invention.

45

50

55

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

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15

(ii) TITLE OF INVENTION: APOPTOSIS-REGULATING PROTEINS

(iii) NUMBER OF SEQUENCES: 35

20

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: Concurrently Herewith
- (C) CLASSIFICATION:

30

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/408,095
- (B) FILING DATE: 21-MAR-1995

35

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ala Pro Ala Pro Gly Phe Phe Ser
1 5

55

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr Arg Arg Asp Phe Ala Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Lys Trp Glu Phe Glu Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Ala Ala Val Ala Phe Leu Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 2

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Tyr Xaa Xaa Xaa Phe Xaa Glu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5

- (ix) FEATURE:
 - (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 Ala Ala Xaa Ala Xaa Phe Xaa Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

 Ala Ala Pro Ala Pro Gly Ile Phe Ser
 1 5

25 (2) INFORMATION FOR SEQ ID NO:8:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
30 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

40 Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
 1 5 10 15

 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
 20 25 30

45 Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 40 45

 Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60

50 Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
 65 70 75 80

55

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
 85 90 95
 5 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110
 Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
 115 120 125
 10 His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140
 Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Arg Gln
 145 150 155 160
 15 Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
 165 170 175

(2) INFORMATION FOR SEQ ID NO:9:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

35

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Ala Ser Leu
 1 5 10 15
 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
 20 25 30
 Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 40 45
 Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60
 45 Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
 65 70 75 80
 Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
 85 90 95
 50 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110

55

Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
 115 120 125
 5 His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140
 Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Arg Gln
 145 150 155 160
 10 Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
 165 170 175

(2) INFORMATION FOR SEQ ID NO:10:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
 1 5 10 15
 30 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Ala Ser Leu Trp
 20 25 30
 Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 35 40 45
 Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60
 40 Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
 65 70 75 80
 Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Ala Val Ala Phe Leu
 85 90 95
 45 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110
 Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
 115 120 125
 50 His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140

55

Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Arg Gln
145 150 155 160

5 Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
165 170 175

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
1 5 10 15

25 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
20 25 30

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
35 40 45

30 Trp Ala Ser Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
50 55 60

Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
35 65 70 75 80

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
85 90 95

40 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
100 105 110

Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
115 120 125

45 His Lys Asn Arg Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
130 135 140

Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Arg Gln
145 150 155 160

50 Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
165 170 175

55

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
 1 5 10 15

Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
 20 25 30

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 40 45

Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60

Leu Asn Leu Gly His Gln Ala Leu Phe Gln Ala Ser Val Ile Lys Thr
 65 70 75 80

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
 85 90 95

Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110

Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
 115 120 125

His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140

Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Gln
 145 150 155 160

Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
 165 170 175

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10

Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
1 5 10 15

Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
20 25 30

15

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
35 40 45

20

Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
50 55 60

Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
65 70 75 80

25

Leu Asp Phe Ser Thr Pro Gly Arg Ala Ser Phe Ile Lys Asp Lys Trp
85 90 95

Ser Glu Glu Thr His Leu Ser Gly Gly Tyr Leu Leu Asp Phe Leu Ala
100 105 110

30

Met His Leu Trp Arg Ala Val Val Arg His Lys Asn Arg Leu Leu Leu
115 120 125

35

Leu Ser Ser Val Arg Pro Ala Ile Ile Pro Thr Glu Glu Gln Gln Gln
130 135 140

Glu Glu Ala Arg Arg Arg Arg Arg Gln Glu Gln Ser Pro Trp Asn Pro
145 150 155 160

40

Arg Ala Gly Leu Asp Pro Arg Glu
165

(2) INFORMATION FOR SEQ ID NO:14:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
 1 5 10 15
 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
 20 25 30
 10 Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 40 45
 Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60
 15 Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
 65 70 75 80
 Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
 85 90 95
 20 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110
 Tyr Leu Leu Asp Phe Leu Ala Met His Leu Ala Ser Ala Val Val Arg
 115 120 125
 25 His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140
 Pro Thr Glu Glu Gln Gln Gln Glu Glu Ala Arg Arg Arg Arg Arg Gln
 145 150 155 160
 Glu Gln Ser Pro Trp Asn Pro Arg Ala Gly Leu Asp Pro Arg Glu
 165 170 175

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

50 Met Glu Ala Trp Glu Cys Leu Glu Asp Phe Ser Ala Val Arg Asn Leu
 1 5 10 15
 Leu Glu Gln Ser Ser Asn Ser Thr Ser Trp Phe Trp Arg Phe Leu Trp
 20 25 30
 55

Gly Ser Ser Gln Ala Lys Leu Val Cys Arg Ile Lys Glu Asp Tyr Lys
 35 40 45
 5 Trp Glu Phe Glu Glu Leu Leu Lys Ser Cys Gly Glu Leu Phe Asp Ser
 50 55 60
 Leu Asn Leu Gly His Gln Ala Leu Phe Gln Glu Lys Val Ile Lys Thr
 65 70 75 80
 10 Leu Asp Phe Ser Thr Pro Gly Arg Ala Ala Ala Val Ala Phe Leu
 85 90 95
 Ser Phe Ile Lys Asp Lys Trp Ser Glu Glu Thr His Leu Ser Gly Gly
 100 105 110
 15 Tyr Leu Leu Asp Phe Leu Ala Met His Leu Trp Arg Ala Val Val Arg
 115 120 125
 His Lys Asn Arg Leu Leu Leu Leu Ser Ser Val Arg Pro Ala Ile Ile
 130 135 140
 20 Pro Thr Ser
 145

25 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 30 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala His Ala Gly Arg Ser Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15
 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30
 45 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Phe
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 50 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80

55

Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
85 90 95

5 Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg Tyr Arg Arg Asp Phe
100 105 110

Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly
115 120 125

10 Cys Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp
130 135 140

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu
145 150 155 160

15 Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp
165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn
180 185 190

20 Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Met Arg Pro
195 200 205

25 Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala
210 215 220

Leu Val Gly Ala Cys Ile Thr Leu Gly Ala Tyr Leu Gly His Lys
225 230 235

30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45

Met Ala His Ala Gly Arg Ser Gly Tyr Asp Asn Arg Glu Ile Val Met
1 5 10 15

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
20 25 30

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Gly Asp Val Gly Ala Ala Pro Pro Gly Phe Ser Ser Gln Pro Gly His
35 40 45

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Thr Pro His Pro Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro
 50 55 60
 5 Leu Gln Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser
 65 70 75 80
 Pro Val Pro Pro Val Val His Leu Thr Leu Arg Gln Ala Gly Asp Asp
 85 90 95
 10 Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu
 100 105 110
 His Leu Thr Pro Phe Thr Ala Arg Gly Cys Phe Ala Thr Val Val Glu
 115 120 125
 15 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
 130 135 140
 Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser
 145 150 155 160
 20 Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg
 165 170 175
 25 His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val
 180 185 190
 Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu
 195 200 205
 30 Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr
 210 215 220
 Leu Gly Ala Tyr Leu Gly His Lys
 225 230
 35

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala His Ala Gly Arg Ser Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15
 55

Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30
 5 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Phe
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 10 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ser
 65 70 75 80
 Pro Val Pro Pro Val Val His Leu Thr Leu Arg Gln Ala Gly Asp Asp
 85 90 95
 15 Phe Ser Arg Arg Tyr Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu
 100 105 110
 20 His Leu Thr Pro Phe Thr Ala Arg Gly Cys Phe Ala Thr Val Val Glu
 115 120 125
 Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe
 130 135 140
 25 Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser
 145 150 155 160
 Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg
 165 170 175
 30 His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val
 180 185 190
 35 Glu Leu Tyr Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu
 195 200 205
 Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr
 210 215 220
 40 Leu Gly Ala Tyr Leu Gly His Lys
 225 230

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 Met Ala His Ala Gly Arg Ser Gly Tyr Asp Asn Arg Glu Ile Val Met
 1 5 10 15
 Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly Tyr Glu Trp Asp Ala
 20 25 30
 10 Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala Pro Ala Pro Gly Phe
 35 40 45
 Phe Ser Ser Gln Pro Gly His Thr Pro His Pro Ala Ala Ser Arg Asp
 50 55 60
 15 Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro Ala Ala Pro Gly Ala
 65 70 75 80
 Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro Val Val His Leu Thr
 85 90 95
 20 Leu Arg Gln Ala Gly Asp Asp Phe Ser Ser Ser Gln Leu His Leu Thr
 100 105 110
 Pro Phe Thr Ala Arg Gly Cys Phe Ala Thr Val Val Glu Glu Leu Phe
 115 120 125
 25 Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly
 130 135 140
 Gly Val Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val
 145 150 155 160
 30 Asp Asn Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His
 165 170 175
 35 Thr Trp Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr
 180 185 190
 Gly Pro Ser Met Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys
 195 200 205
 40 Thr Leu Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Ala
 210 215 220
 Tyr Leu Gly His Lys
 225

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 11..694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

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AGTCCCAAC ATG GCG GCT CCC CAA GAC GTC CAC GTC CGG ATC TGT AAC 49
 Met Ala Ala Pro Gln Asp Val His Val Arg Ile Cys Asn
 1 5 10

CAA GAG ATT GTC AAA TTT GAC CTG GAG GTG AAG GCG CTT ATT CAG GAT 97
 Gln Glu Ile Val Lys Phe Asp Leu Glu Val Lys Ala Leu Ile Gln Asp
 15 20 25

ATC CGT GAT TGT TCA GGA CCC TTA AGT GCT CTT ACT GAA CTG AAT ACT 145
 Ile Arg Asp Cys Ser Gly Pro Leu Ser Ala Leu Thr Glu Leu Asn Thr
 30 35 40 45

AAA GTA AAA GAG AAA TTT CAA CAG TTG CGT CAC AGA ATA CAG GAC CTG 193
 Lys Val Lys Glu Lys Phe Gln Gln Leu Arg His Arg Ile Gln Asp Leu
 50 55 60

GAG CAG TTG GCT AAA GAG CAA GAC AAA GAA TCA GAG AAA CAA CTT CTA 241
 Glu Gln Leu Ala Lys Glu Gln Asp Lys Glu Ser Glu Lys Gln Leu Leu
 65 70 75

CTC CAG GAA GTG GAG AAT CAC AAA AAG CAG ATG CTC AGC AAT CAG GCC 289
 Leu Gln Glu Val Glu Asn His Lys Lys Gln Met Leu Ser Asn Gln Ala
 80 85 90

TCA TGG AGG AAA GCT AAT CTC ACC TGC AAA ATT GCA ATC GAC AAT CTA 337
 Ser Trp Arg Lys Ala Asn Leu Thr Cys Lys Ile Ala Ile Asp Asn Leu
 95 100 105

GAG AAA GCA GAA CTT CTT CAG GGA GGA GAT CTC TTA AGG CAA AGG AAA 385
 Glu Lys Ala Glu Leu Leu Gln Gly Gly Asp Leu Leu Arg Gln Arg Lys
 110 115 120 125

ACC ACC AAA GAG AGC CTG GCC CAG ACA TCC AGT ACC ATC ACT GAG AGC 433
 Thr Thr Lys Glu Ser Leu Ala Gln Thr Ser Ser Thr Ile Thr Glu Ser
 130 135 140

CTC ATG GGG ATC AGC AGG ATG ATG GCC CAG CAG GTC CAG CAG AGC GAG 481
 Leu Met Gly Ile Ser Arg Met Met Ala Gln Gln Val Gln Gln Ser Glu
 145 150 155

GAG GCC ATG CAG TCT CTA GTC ACT TCT TCA CGA ACG ATC CTG GAT GCA 529
 Glu Ala Met Gln Ser Leu Val Thr Ser Ser Arg Thr Ile Leu Asp Ala
 160 165 170

AAT GAA GAA TTT AAG TCC ATG TCG GGC ACC ATC CAG CTG GGC CGG AAG 577
 Asn Glu Glu Phe Lys Ser Met Ser Gly Thr Ile Gln Leu Gly Arg Lys
 175 180 185
 5 CTT ATC ACA AAA TAC AAT CGC CGG GAG CTG ACG GAC AAG CTT CTC ATC 625
 Leu Ile Thr Lys Tyr Asn Arg Arg Glu Leu Thr Asp Lys Leu Leu Ile
 190 195 200 205
 10 TTC CTT GCG CTA CGC CTG TTT CTT GCT ACG GTC CTC TAT ATT GTG AAA 673
 Phe Leu Ala Leu Arg Leu Phe Leu Ala Thr Val Leu Tyr Ile Val Lys
 210 215 220
 AAG CGG CTC TTT CCA TTT TTG TGAGATCCCA AAGGTGCCAG TTCTGGCCCT 724
 Lys Arg Leu Phe Pro Phe Leu
 15 225
 TTCAGCTCCT GTTTCAGGAT CTGTCCTGGT TCCTGAGCTC TAGGCTGCTA AGCTGAGCCA 784
 CACACCCCTC CGTTTTGCAC CAGTTGCCTG CAGGTTGGAT GGAACACAGT GCCCCACTTT 844
 20 TCTGCAAGTA GCTGGCTTGT AAAGGGTGAA CAGAGCCATG GGAGGAAGGT CTGGCATTGG 904
 GATGCCGCCC TGGGGACATA CGAACCGCCT CCTTCCACCA TTGTGCACTA TGGGAGGCCG 964
 CTGCTGCGTG GAGCACTTAA AGTCCAGCCT CCAGGACCGG ATGCCCCTCC TGTCTCCCGC 1024
 25 TCCCATCGTG CCCTTAAATG CCAGATCTGG TGGAGGGAAG AGAGAAGAGG TAGGAAGAAA 1084
 GGTGATGAAA ACTCCTG 1101
 30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 228 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ala Ala Pro Gln Asp Val His Val Arg Ile Cys Asn Gln Glu Ile
 1 5 10 15
 45 Val Lys Phe Asp Leu Glu Val Lys Ala Leu Ile Gln Asp Ile Arg Asp
 20 25 30
 Cys Ser Gly Pro Leu Ser Ala Leu Thr Glu Leu Asn Thr Lys Val Lys
 35 40 45
 50 Glu Lys Phe Gln Gln Leu Arg His Arg Ile Gln Asp Leu Glu Gln Leu
 50 55 60

55

Ala Lys Glu Gln Asp Lys Glu Ser Glu Lys Gln Leu Leu Leu Gln Glu
65 70 75 80

5 Val Glu Asn His Lys Lys Gln Met Leu Ser Asn Gln Ala Ser Trp Arg
85 90 95

Lys Ala Asn Leu Thr Cys Lys Ile Ala Ile Asp Asn Leu Glu Lys Ala
100 105 110

10 Glu Leu Leu Gln Gly Gly Asp Leu Leu Arg Gln Arg Lys Thr Thr Lys
115 120 125

Glu Ser Leu Ala Gln Thr Ser Ser Thr Ile Thr Glu Ser Leu Met Gly
130 135 140

15 Ile Ser Arg Met Met Ala Gln Gln Val Gln Gln Ser Glu Glu Ala Met
145 150 155 160

Gln Ser Leu Val Thr Ser Ser Arg Thr Ile Leu Asp Ala Asn Glu Glu
165 170 175

20 Phe Lys Ser Met Ser Gly Thr Ile Gln Leu Gly Arg Lys Leu Ile Thr
180 185 190

25 Lys Tyr Asn Arg Arg Glu Leu Thr Asp Lys Leu Leu Ile Phe Leu Ala
195 200 205

Leu Arg Leu Phe Leu Ala Thr Val Leu Tyr Ile Val Lys Lys Arg Leu
210 215 220

30 Phe Pro Phe Leu
225

(2) INFORMATION FOR SEQ ID NO:22:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
45 (A) NAME/KEY: CDS
(B) LOCATION: 214..1155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

50 CTGCGGCCGG GGGATTGGGC CGGGTCTCC ACCGCCGACC GAGGGGAGCG GCGTCCGCTC 60
GGCCCTGCTT TTTGCGACCT GCCGTCAGCC CCACGTCGCC GGCCTGGAGG GCGAAGAGG 120

55

	ACGAGGGGCG ACGAAGGCCC AAGGCTTCCT CCGGGGACAT TGGCTCCCTG GATTATCAAG	180
	CAGTTTGTAG TTGACATTGA ATCCAGGCTG AGG ATG GAA GGT GTG GAA CTT AAA	234
5	Met Glu Gly Val Glu Leu Lys 230 235	
	GAA GAA TGG CAA GAT GAA GAT TTT CCG ATA CCT TTA CCA GAA GAT GAT	282
	Glu Glu Trp Gln Asp Glu Asp Phe Pro Ile Pro Leu Pro Glu Asp Asp	
10	240 245 250	
	AGT ATT GAA GCA GAT ATA CTA GCT ATA ACT GGA CCA GAG GAC CAG CCT	330
	Ser Ile Glu Ala Asp Ile Leu Ala Ile Thr Gly Pro Glu Asp Gln Pro	
	255 260 265	
15	GGC TCA CTA GAA GTT AAT GGA AAT AAA GTG AGA AAG AAA CTA ATG GCT	378
	Gly Ser Leu Glu Val Asn Gly Asn Lys Val Arg Lys Lys Leu Met Ala	
	270 275 280	
	CCA GAC ATT AGC CTG ACA CTG GAT CCT AGT GAT GGC TCT GTA TTG TCA	426
20	Pro Asp Ile Ser Leu Thr Leu Asp Pro Ser Asp Gly Ser Val Leu Ser	
	285 290 295	
	GAT GAT TTG GAT GAA AGT GGG GAG ATT GAC TTA GAT GGC TTA GAC ACA	474
	Asp Asp Leu Asp Glu Ser Gly Glu Ile Asp Leu Asp Gly Leu Asp Thr	
25	300 305 310 315	
	CCG TCA GAG AAT AGT AAT GAG TTT GAG TGG GAA GAT GAT CTT CCA AAA	522
	Pro Ser Glu Asn Ser Asn Glu Phe Glu Trp Glu Asp Asp Leu Pro Lys	
	320 325 330	
30	CCC AAG ACT ACT GAA GTA ATT AGG AAA GGC TCA ATT ACT GAA TAC ACA	570
	Pro Lys Thr Thr Glu Val Ile Arg Lys Gly Ser Ile Thr Glu Tyr Thr	
	335 340 345	
	GCA GCA GAG GAA AAA GAA GAT GGA CGA CGC TGG CGT ATG TTC AGG ATT	618
35	Ala Ala Glu Glu Lys Glu Asp Gly Arg Arg Trp Arg Met Phe Arg Ile	
	350 355 360	
	GGA GAA CAG GAC CAC AGG GTT GAT ATG AAG GCA ATT GAA CCC TAT AAA	666
	Gly Glu Gln Asp His Arg Val Asp Met Lys Ala Ile Glu Pro Tyr Lys	
40	365 370 375	
	AAA GTT ATC AGC CAT GGG GGA TAT TAT GGG GAT GGA TTA AAT GCC ATT	714
	Lys Val Ile Ser His Gly Gly Tyr Tyr Gly Asp Gly Leu Asn Ala Ile	
	380 385 390 395	
45	GTT GTA TTT GCT GTC TGT TTC ATG CCT GAA AGT AGT CAG CCT AAC TAT	762
	Val Val Phe Ala Val Cys Phe Met Pro Glu Ser Ser Gln Pro Asn Tyr	
	400 405 410	
50	AGA TAC CTG ATG GAC AAT CTT TTT AAA TAT GTT ATT GGC ACT TTG GAG	810
	Arg Tyr Leu Met Asp Asn Leu Phe Lys Tyr Val Ile Gly Thr Leu Glu	
	415 420 425	

55

	CTA TTA GTA GCA GAA AAC TAC ATG ATA GTT TAT TTA AAT GGT GCA ACA	858
	Leu Leu Val Ala Glu Asn Tyr Met Ile Val Tyr Leu Asn Gly Ala Thr	
	430 435 440	
5	ACT CGA AGA AAA ATG CCC AGT CTG GGA TGG CTC AGG AAA TGT TAT CAG	906
	Thr Arg Arg Lys Met Pro Ser Leu Gly Trp Leu Arg Lys Cys Tyr Gln	
	445 450 455	
10	CAA ATT GAT AGA AGG TTA CGG AAA AAT CTA AAA TCC CTA ATC ATT GTA	954
	Gln Ile Asp Arg Arg Leu Arg Lys Asn Leu Lys Ser Leu Ile Ile Val	
	460 465 470 475	
	CAT CCT TCT TGG TTT ATC AGA ACA CTT CTG GCT GTT ACA AGA CCA TTT	1002
15	His Pro Ser Trp Phe Ile Arg Thr Leu Ala Val Thr Arg Pro Phe	
	480 485 490	
	ATT AGC TCG AAA TTC AGC CAA AAA ATT AGA TAC GTG TTT AAT TTG GCA	1050
	Ile Ser Ser Lys Phe Ser Gln Lys Ile Arg Tyr Val Phe Asn Leu Ala	
	495 500 505	
20	GAA CTA GCA GAA CTT GTC CCC ATG GAA TAC GTT GGC ATA CCA GAA TGC	1098
	Glu Leu Ala Glu Leu Val Pro Met Glu Tyr Val Gly Ile Pro Glu Cys	
	510 515 520	
25	ATA AAA CAA GTT GAT CAA GAA CTT AAT GGA AAA CAA GAT GAA CCG AAA	1146
	Ile Lys Gln Val Asp Gln Glu Leu Asn Gly Lys Gln Asp Glu Pro Lys	
	525 530 535	
	AAT GAA CAG TAAGTTTGGC ATCTAGTCCA AACAAGACTG AAGAATGTGC	1195
30	Asn Glu Gln	
	540	
	TGATGGAGCA GTGCTGTTTC TGCATTCATA ATGCATTTAT TGGCCATATT TTTATGTAAC	1255
	CTGTTACAAA ATAGACTTGA CTTTTTCATA ATGGACTTTT GTATTATACA AGGGACTGTT	1315
35	CACTGCTGTA CTGGTTTGCA AATTTCTTGA ATTTAGCTCT TTATGCTAAC TGTATTATTA	1375
	TCATTTTATA T	1386
40	(2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 314 amino acids	
45	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
50	Met Glu Gly Val Glu Leu Lys Glu Glu Trp Gln Asp Glu Asp Phe Pro	
	1 5 10 15	
55		

Ile Pro Leu Pro Glu Asp Asp Ser Ile Glu Ala Asp Ile Leu Ala Ile
 20 25 30
 5 Thr Gly Pro Glu Asp Gln Pro Gly Ser Leu Glu Val Asn Gly Asn Lys
 35 40 45
 Val Arg Lys Lys Leu Met Ala Pro Asp Ile Ser Leu Thr Leu Asp Pro
 50 55 60
 10 Ser Asp Gly Ser Val Leu Ser Asp Asp Leu Asp Glu Ser Gly Glu Ile
 65 70 75 80
 Asp Leu Asp Gly Leu Asp Thr Pro Ser Glu Asn Ser Asn Glu Phe Glu
 85 90 95
 15 Trp Glu Asp Asp Leu Pro Lys Pro Lys Thr Thr Glu Val Ile Arg Lys
 100 105 110
 Gly Ser Ile Thr Glu Tyr Thr Ala Ala Glu Glu Lys Glu Asp Gly Arg
 115 120 125
 20 Arg Trp Arg Met Phe Arg Ile Gly Glu Gln Asp His Arg Val Asp Met
 130 135 140
 25 Lys Ala Ile Glu Pro Tyr Lys Lys Val Ile Ser His Gly Gly Tyr Tyr
 145 150 155 160
 Gly Asp Gly Leu Asn Ala Ile Val Val Phe Ala Val Cys Phe Met Pro
 165 170 175
 30 Glu Ser Ser Gln Pro Asn Tyr Arg Tyr Leu Met Asp Asn Leu Phe Lys
 180 185 190
 Tyr Val Ile Gly Thr Leu Glu Leu Leu Val Ala Glu Asn Tyr Met Ile
 195 200 205
 35 Val Tyr Leu Asn Gly Ala Thr Thr Arg Arg Lys Met Pro Ser Leu Gly
 210 215 220
 Trp Leu Arg Lys Cys Tyr Gln Gln Ile Asp Arg Arg Leu Arg Lys Asn
 225 230 235 240
 Leu Lys Ser Leu Ile Ile Val His Pro Ser Trp Phe Ile Arg Thr Leu
 245 250 255
 45 Leu Ala Val Thr Arg Pro Phe Ile Ser Ser Lys Phe Ser Gln Lys Ile
 260 265 270
 Arg Tyr Val Phe Asn Leu Ala Glu Leu Ala Glu Leu Val Pro Met Glu
 275 280 285
 50 Tyr Val Gly Ile Pro Glu Cys Ile Lys Gln Val Asp Gln Glu Leu Asn
 290 295 300

55

Gly Lys Gln Asp Glu Pro Lys Asn Glu Gln
305 310

6 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 826 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 109..690

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

	AAAGAGATCT GGAATTCGGA TCCTCGAGGC CACGAAGGCC ACCGCCCGCA GCTGAAGCAC	60
	ATCCGCAGCC CGGCGCGACT CCGATCGCCG CAGTTGCCCT CTGGCGCC ATG TCC GAG	117
25	Met Ser Glu 315	
	AAC GGA GCG CCC GGG ATG CAG GAG GAG AGC CTG CAG GGC TCC TGG GTA	165
	Asn Gly Ala Pro Gly Met Gln Glu Ser Leu Gln Gly Ser Trp Val	
30	320 325 330	
	GAA CTG CAC TTC AGC AAT AAT GGG AAC GGG GGC AGC GTT CCA GCC TCG	213
	Glu Leu His Phe Ser Asn Asn Gly Asn Gly Gly Ser Val Pro Ala Ser	
	335 340 345	
35	GTT TCT ATT TAT AAT GGA GAC ATG GAA AAA ATA CTG CTG GAC GCA CAG	261
	Val Ser Ile Tyr Asn Gly Asp Met Glu Lys Ile Leu Leu Asp Ala Gln	
	350 355 360 365	
	CAT GAG TCT GGA CGG AGT AGC TCC AAG AGC TCT CAC TGT GAC AGC CCA	309
40	His Glu Ser Gly Arg Ser Ser Ser Lys Ser Ser His Cys Asp Ser Pro	
	370 375 380	
	CCT CGC TCG CAG ACA CCA CAA GAT ACC AAC AGG GCT TCT GAA ACA GAT	357
	Pro Arg Ser Gln Thr Pro Gln Asp Thr Asn Arg Ala Ser Glu Thr Asp	
45	385 390 395	
	ACC CAT AGC ATT GGA GAG AAA AAC AGC TCA CAG TCT GAG GAA GAT GAT	405
	Thr His Ser Ile Gly Glu Lys Asn Ser Ser Gln Ser Glu Glu Asp Asp	
	400 405 410	
50	ATT GAA AGA AGG AAA GAA GTT GAA AGC ATC TTG AAG AAA AAC TCA GAT	453
	Ile Glu Arg Arg Lys Glu Val Glu Ser Ile Leu Lys Lys Asn Ser Asp	
	415 420 425	

55

TGG ATA TGG GAT TGG TCA AGT CGG CCG GAA AAT ATT CCC CCC AAG GAG 501
 Trp Ile Trp Asp Trp Ser Ser Arg Pro Glu Asn Ile Pro Pro Lys Glu
 430 435 440 445
 5
 TTC CTC TTT AAA CAC CCG AAG CGC ACG GCC ACC CTC AGC ATG AGG AAC 549
 Phe Leu Phe Lys His Pro Lys Arg Thr Ala Thr Leu Ser Met Arg Asn
 450 455 460
 10
 ACG AGC GTC ATG AAG AAA GGG GGC ATA TTC TCT GCA GAA TTT CTG AAA 597
 Thr Ser Val Met Lys Lys Gly Gly Ile Phe Ser Ala Glu Phe Leu Lys
 465 470 475
 GTT TTC CTT CCA TCT CTG CTG CTC TCT CAT TTG CTG GCC ATC GGA TTG 645
 Val Phe Leu Pro Ser Leu Leu Leu Ser His Leu Leu Ala Ile Gly Leu
 15 480 485 490
 GGG ATC TAT ATT GGA AGG CGT CTG ACA ACC TCC ACC AGC ACC TTT 690
 Gly Ile Tyr Ile Gly Arg Arg Leu Thr Thr Ser Thr Ser Thr Phe
 495 500 505
 20
 TGATGAAGAA CTGGAGTCTG ACTTGGTTTCG TTAGTGGATT ACTTCTGAGC TTGCAACATA 750
 GCTCACTGAA GAGCTGTTAG ATCCTGGGCC TTCGTGGCTC GAGAGACTAG AATCGCAGAT 810
 ACGAAAACCC CGCAGC 826
 25

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Ser Glu Asn Gly Ala Pro Gly Met Gln Glu Glu Ser Leu Gln Gly
 1 5 10 15
 40 Ser Trp Val Glu Leu His Phe Ser Asn Asn Gly Asn Gly Gly Ser Val
 20 25 30
 Pro Ala Ser Val Ser Ile Tyr Asn Gly Asp Met Glu Lys Ile Leu Leu
 35 40 45
 45 Asp Ala Gln His Glu Ser Gly Arg Ser Ser Ser Lys Ser Ser His Cys
 50 55 60
 Asp Ser Pro Pro Arg Ser Gln Thr Pro Gln Asp Thr Asn Arg Ala Ser
 50 65 70 75 80
 Glu Thr Asp Thr His Ser Ile Gly Glu Lys Asn Ser Ser Gln Ser Glu
 85 90 95

55

Glu Asp Asp Ile Glu Arg Arg Lys Glu Val Glu Ser Ile Leu Lys Lys
 100 105 110
 5 Asn Ser Asp Trp Ile Trp Asp Trp Ser Ser Arg Pro Glu Asn Ile Pro
 115 120 125
 Pro Lys Glu Phe Leu Phe Lys His Pro Lys Arg Thr Ala Thr Leu Ser
 130 135 140
 10 Met Arg Asn Thr Ser Val Met Lys Lys Gly Gly Ile Phe Ser Ala Glu
 145 150 155 160
 Phe Leu Lys Val Phe Leu Pro Ser Leu Leu Leu Ser His Leu Leu Ala
 165 170 175
 15 Ile Gly Leu Gly Ile Tyr Ile Gly Arg Arg Leu Thr Thr Ser Thr Ser
 180 185 190
 Thr Phe
 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 946 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 25

(ii) MOLECULE TYPE: cDNA
30

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 26..505
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAGCATCGCC GCCGCCAGAG GAGAA ATG TCT GAA GTA AGA CCC CTC TCC AGA 52
 40 Met Ser Glu Val Arg Pro Leu Ser Arg
 195 200
 GAC ATC TTG ATG GAG ACC CTC CTG TAT GAG CAG CTC CTG GAA CCC CCG 100
 45 Asp Ile Leu Met Glu Thr Leu Leu Tyr Glu Gln Leu Leu Glu Pro Pro
 205 210 215
 ACC ATG GAG GTT CTT GGC ATG ACT GAC TCT GAA GAG GAC CTG GAC CCT 148
 Thr Met Glu Val Leu Gly Met Thr Asp Ser Glu Glu Asp Leu Asp Pro
 220 225 230 235
 50 ATG GAG GAC TTC GAT TCT TTG GAA TGC ATG GAG GGC AGT GAC GCA TTG 196
 Met Glu Asp Phe Asp Ser Leu Glu Cys Met Glu Gly Ser Asp Ala Leu
 240 245 250

55

5 GCC CTG CCG CTG GCC TGC ATC GGG GAC GAG ATG GAC GTG AGC CTC AGG 244
 Ala Leu Arg Leu Ala Cys Ile Gly Asp Glu Met Asp Val Ser Leu Arg
 255 260 265

10 GCC CCG CGC CTG GCC CAG CTC TCC GAG GTG GCC ATG CAC AGC CTG GGT 292
 Ala Pro Arg Leu Ala Gln Leu Ser Glu Val Ala Met His Ser Leu Gly
 270 275 280

15 CTG GCT TTC ATC TAC GAC CAG ACT GAG GAC ATC AGG GAT GTT CTT AGA 340
 Leu Ala Phe Ile Tyr Asp Gln Thr Glu Asp Ile Arg Asp Val Leu Arg
 285 290 295

20 AGT TTC ATG GAC GGT TTC ACC ACA CTT AAG GAG AAC ATA ATG AGG TTC 388
 Ser Phe Met Asp Gly Phe Thr Thr Leu Lys Glu Asn Ile Met Arg Phe
 300 305 310 315

25 TGG AGA TCC CCG AAC CCC GGG TCC TGG GTG TCC TGC GAA CAG GTG CTG 436
 Trp Arg Ser Pro Asn Pro Gly Ser Trp Val Ser Cys Glu Gln Val Leu
 320 325 330

30 CTG GCG CTG CTG CTG CTG CTG GCG CTG CTG CTG CCG CTG CTC AGC GGG 484
 Leu Ala Leu Leu Leu Leu Leu Ala Leu Leu Leu Pro Leu Leu Ser Gly
 335 340 345

35 GGC CTG CAC CTG CTG CTC AAG TGAGGCCCG GCGGCTCAGG GCGTGGCTGG 535
 Gly Leu His Leu Leu Leu Lys
 350

40 CCCCACCCCC ATGACCACTG CCCTGGAGGT GGCGGCCTGC TGCTGTTATC TTTTAACTG 595
 TTTTCTCATG ATGCCTTTTT ATATTTAAAC CCCGAGATAG TGCTGGAACA CTGCTGAGGT 655
 TTTATACTCA GGTTTTTTGT TTTTTTTT TA TCCAGTTTT CGTTTTTTCT AAAAGATGAA 715

45 TTCCTATGGC TCTGCAATTG TCACCGGTTA ACTGTGGCCT GTGCCCAGGA AGAGCCATTC 775
 ACTCCTGCCC CTGCCCACAC GGCAGGTAGC AGGGGGAGTG CTGGTCACAC CCCTGTGTGA 835
 TATGTGATGC CCTCGGCAAA GAATCTACTG GAATAGATTC CGAGGAGCAG GAGTGCTCAA 895

50 TAAAATGTTG GTTTCAGCA AAAAAAAAAA AAAGGCCTTC GTGGCCTCGA G 946

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

5 Met Ser Glu Val Arg Pro Leu Ser Arg Asp Ile Leu Met Glu Thr Leu
 1 5 10 15
 Leu Tyr Glu Gln Leu Leu Glu Pro Pro Thr Met Glu Val Leu Gly Met
 20 25 30
 10 Thr Asp Ser Glu Glu Asp Leu Asp Pro Met Glu Asp Phe Asp Ser Leu
 35 40 45
 Glu Cys Met Glu Gly Ser Asp Ala Leu Ala Leu Arg Leu Ala Cys Ile
 50 55 60
 15 Gly Asp Glu Met Asp Val Ser Leu Arg Ala Pro Arg Leu Ala Gln Leu
 65 70 75 80
 Ser Glu Val Ala Met His Ser Leu Gly Leu Ala Phe Ile Tyr Asp Gln
 85 90 95
 20 Thr Glu Asp Ile Arg Asp Val Leu Arg Ser Phe Met Asp Gly Phe Thr
 100 105 110
 Thr Leu Lys Glu Asn Ile Met Arg Phe Trp Arg Ser Pro Asn Pro Gly
 115 120 125
 25 Ser Trp Val Ser Cys Glu Gln Val Leu Leu Ala Leu Leu Leu Leu
 130 135 140
 Ala Leu Leu Leu Pro Leu Leu Ser Gly Gly Leu His Leu Leu Leu Lys
 145 150 155 160
 30

(2) INFORMATION FOR SEQ ID NO:28:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 981 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 45 (A) NAME/KEY: CDS
 (B) LOCATION: 1..777

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

50 ATG GAC GCC TGG GTC CGC TTC AGT GCT CAG AGC CAA GCC CGG GAG CGG
 Met Asp Ala Trp Val Arg Phe Ser Ala Gln Ser Gln Ala Arg Glu Arg
 165 170 175
 55

48

	CTG TGT AGG GCC GCC CAG TAT GCT TGC TCT CTT CTT GGC CAT GCG CTG	96
	Leu Cys Arg Ala Ala Gln Tyr Ala Cys Ser Leu Leu Gly His Ala Leu	
	180 185 190	
5	CAG AGG CAT GGA GCC AGT CCT GAG TTA CAG AAA CAG ATT CGA CAA CTG	144
	Gln Arg His Gly Ala Ser Pro Glu Leu Gln Lys Gln Ile Arg Gln Leu	
	195 200 205	
10	GAG AGC CAC CTG AGC CTT GGA AGA AAG CTT CTA CGC CTG GGT AAC TCA	192
	Glu Ser His Leu Ser Leu Gly Arg Lys Leu Leu Arg Leu Gly Asn Ser	
	210 215 220	
	GCA GAT GCC CTT GAG TCA GCC AAA AGA GCT GTT CAC CTA TCA GAT GTT	240
	Ala Asp Ala Leu Glu Ser Ala Lys Arg Ala Val His Leu Ser Asp Val	
15	225 230 235 240	
	GTC CTG AGA TTC TGC ATC ACT GTT AGT CAC CTC AAT CGA GCC TTG TAC	288
	Val Leu Arg Phe Cys Ile Thr Val Ser His Leu Asn Arg Ala Leu Tyr	
	245 250 255	
20	TTC GCC TGT CAC AAT GTC CTG TGG GCT GGA AAG TCT GGA CTG GCT CCC	336
	Phe Ala Cys His Asn Val Leu Trp Ala Gly Lys Ser Gly Leu Ala Pro	
	260 265 270	
25	CGT GTG GAT CAG GAG AAG TGG GCC CAG CGT TCA TTC AGG TAC TAT TTG	384
	Arg Val Asp Gln Glu Lys Trp Ala Gln Arg Ser Phe Arg Tyr Tyr Leu	
	275 280 285	
	TTT TCC CTC ATC ATG AAT TTG AGC CGT GAT GCT TAT GAG ATT CGC CTA	432
	Phe Ser Leu Ile Met Asn Leu Ser Arg Asp Ala Tyr Glu Ile Arg Leu	
30	290 295 300	
	CTG ATG GAG CAA GAG TCT TCT GCT TGT AGC CGG CGA CTG AAA GGT TCT	480
	Leu Met Glu Gln Glu Ser Ser Ala Cys Ser Arg Arg Leu Lys Gly Ser	
	305 310 315 320	
35	GGA GGA GGA GTC CCA GGA GGA AGT GAA ACT GGG GGA CTT GGG GGA CCA	528
	Gly Gly Gly Val Pro Gly Gly Ser Glu Thr Gly Gly Leu Gly Gly Pro	
	325 330 335	
	GGG ACT CCA GGA GGA GGT CTG CCC CAA CTG GCT CTG AAA CTT CGG CTG	576
40	Gly Thr Pro Gly Gly Gly Leu Pro Gln Leu Ala Leu Lys Leu Arg Leu	
	340 345 350	
	CAA GTC CTG CTC CTG GCT CGA GTC CTT AGA GGT CAT CCC CCA CTT CTG	624
	Gln Val Leu Leu Leu Ala Arg Val Leu Arg Gly His Pro Pro Leu Leu	
45	355 360 365	
	CTA GAC GTG GTC AGA AAT GCC TGT GAT CTC TTC ATT CCT CTG GAC AAA	672
	Leu Asp Val Val Arg Asn Ala Cys Asp Leu Phe Ile Pro Leu Asp Lys	
	370 375 380	
50	CTA GCG CTC TGG CGC TGT GGC CCT GGG ATT GTG GGG CTT TGT GGC CTC	720
	Leu Ala Leu Trp Arg Cys Gly Pro Gly Ile Val Gly Leu Cys Gly Leu	
	385 390 395 400	
55		

GTG TCC TCC ATC CTG TCT ATT CTC ACC CTA ATC TAT CCC TGG CTA CGA 768
 Val Ser Ser Ile Leu Ser Ile Leu Thr Leu Ile Tyr Pro Trp Leu Arg
 405 410 415

6

CTC AAG CCC TGACTTCCGG TACAGGATAA GGAGGGGACC TGAATTGGTG 817
 Leu Lys Pro

10

AGATGGAATC TTAGATCGTC CCCATGTGCC AGCCTCATTC GAATTCTACT CTTTGGTTAA 877
 AGTTAGAAAT TCAGAGATTT AGGGGTGGAG GAGGAAGAGC TTTGGGGAAG ATGAGGTAAG 937
 GAAAGATGAC TCGTGAAGTT AATAGGATGT CTCTAATTTC TAGA 981

15

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Asp Ala Trp Val Arg Phe Ser Ala Gln Ser Gln Ala Arg Glu Arg
 1 5 10 15
 Leu Cys Arg Ala Ala Gln Tyr Ala Cys Ser Leu Leu Gly His Ala Leu
 20 25 30
 Gln Arg His Gly Ala Ser Pro Glu Leu Gln Lys Gln Ile Arg Gln Leu
 35 40 45
 Glu Ser His Leu Ser Leu Gly Arg Lys Leu Leu Arg Leu Gly Asn Ser
 50 55 60
 Ala Asp Ala Leu Glu Ser Ala Lys Arg Ala Val His Leu Ser Asp Val
 40 65 70 75 80
 Val Leu Arg Phe Cys Ile Thr Val Ser His Leu Asn Arg Ala Leu Tyr
 85 90 95
 Phe Ala Cys His Asn Val Leu Trp Ala Gly Lys Ser Gly Leu Ala Pro
 45 100 105 110
 Arg Val Asp Gln Glu Lys Trp Ala Gln Arg Ser Phe Arg Tyr Tyr Leu
 115 120 125
 Phe Ser Leu Ile Met Asn Leu Ser Arg Asp Ala Tyr Glu Ile Arg Leu
 130 135 140

50

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Leu Met Glu Gln Glu Ser Ser Ala Cys Ser Arg Arg Leu Lys Gly Ser
 145 150 155 160
 5 Gly Gly Gly Val Pro Gly Gly Ser Glu Thr Gly Gly Leu Gly Gly Pro
 165 170 175
 Gly Thr Pro Gly Gly Gly Leu Pro Gln Leu Ala Leu Lys Leu Arg Leu
 180 185 190
 10 Gln Val Leu Leu Leu Ala Arg Val Leu Arg Gly His Pro Pro Leu Leu
 195 200 205
 Leu Asp Val Val Arg Asn Ala Cys Asp Leu Phe Ile Pro Leu Asp Lys
 210 215 220
 15 Leu Ala Leu Trp Arg Cys Gly Pro Gly Ile Val Gly Leu Cys Gly Leu
 225 230 235 240
 Val Ser Ser Ile Leu Ser Ile Leu Thr Leu Ile Tyr Pro Trp Leu Arg
 20 245 250 255
 Leu Lys Pro

25 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2166 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1503

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGT CAA GTC GAG TTT CTT TGC ATG TCA CTG GCC AAT CCT CTT CCA ACA	48
Ser Gln Val Glu Phe Leu Cys Met Ser Leu Ala Asn Pro Leu Pro Thr	
260 265 270 275	
45 AAT TAC ACG TGG TAC CAC AAT GGG AAA GAA ATG CAG GGA AGG ACA GAG	96
Asn Tyr Thr Trp Tyr His Asn Gly Lys Glu Met Gln Gly Arg Thr Glu	
280 285 290	
50 GAG AAA GTC CAC ATC CCA AAG ATC CTC CCC TGG CAC GCT GGG ACT TAT	144
Glu Lys Val His Ile Pro Lys Ile Leu Pro Trp His Ala Gly Thr Tyr	
295 300 305	

55

	TCC TGT GTG GCA GAA AAC ATT CTT GGT ACT GGA CAG AGG GGC CCG GGA Ser Cys Val Ala Glu Asn Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly 310 315 320	192
5	GCT GAG CTG GAT GTC CAG TAT CCT CCC AAG AAG GTG ACC ACA GTG ATT Ala Glu Leu Asp Val Gln Tyr Pro Pro Lys Lys Val Thr Thr Val Ile 325 330 335	240
10	CAA AAC CCC ATG CCG ATT CGA GAA GGA GAC ACA GTG ACC CTT TCC TGT Gln Asn Pro Met Pro Ile Arg Glu Gly Asp Thr Val Thr Leu Ser Cys 340 345 350 355	288
15	AAC TAC AAT TCC AGT AAC CCC AGT GTT ACC CGG TAT GAA TGG AAA CCC Asn Tyr Asn Ser Ser Asn Pro Ser Val Thr Arg Tyr Glu Trp Lys Pro 360 365 370	336
	CAT GGC GCC TGG GAG GAG CCA TCG CTT GGG GTG CTG AAG ATC CAA AAC His Gly Ala Trp Glu Glu Pro Ser Leu Gly Val Leu Lys Ile Gln Asn 375 380 385	384
20	GTT GGC TGG GAC AAC ACA ACC ATC GCC TGC GCA CGT TGT AAT AGT TGG Val Gly Trp Asp Asn Thr Thr Ile Ala Cys Ala Arg Cys Asn Ser Trp 390 395 400	432
25	TGC TCG TGG GCC TCC CCT GTC GCC CTG AAT GTC CAG TAT GCC CCC CGA Cys Ser Trp Ala Ser Pro Val Ala Leu Asn Val Gln Tyr Ala Pro Arg 405 410 415	480
30	GAC GTG AGG GTC CGG AAA ATC AAG CCC CTT TCC GAG ATT CAC TCT GGA Asp Val Arg Val Arg Lys Ile Lys Pro Leu Ser Glu Ile His Ser Gly 420 425 430 435	528
	AAC TCG GTC AGC CTC CAA TGT GAC TTC TCA AGC AGC CAC CCC AAA GAA Asn Ser Val Ser Leu Gln Cys Asp Phe Ser Ser Ser His Pro Lys Glu 440 445 450	576
35	GTC CAG TTC TTC TGG GAG AAA AAT GGC AGG CTT CTG GGG AAA GAA AGC Val Gln Phe Phe Trp Glu Lys Asn Gly Arg Leu Leu Gly Lys Glu Ser 455 460 465	624
40	CAG CTG AAT TTT GAC TCC ATC TCC CCA GAA GAT GCT GGG AGT TAC AGC Gln Leu Asn Phe Asp Ser Ile Ser Pro Glu Asp Ala Gly Ser Tyr Ser 470 475 480	672
45	TGC TGG GTG AAC AAC TCC ATA GGA CAG ACA GCG TCC AAG GCC TGG ACA Cys Trp Val Asn Asn Ser Ile Gly Gln Thr Ala Ser Lys Ala Trp Thr 485 490 495	720
	CTT GAA GTG CTG TAT GCA CCC AGG AGG CTG CGT GTG TCC ATG AGC CCG Leu Glu Val Leu Tyr Ala Pro Arg Arg Leu Arg Val Ser Met Ser Pro 500 505 510 515	768
50	GGG GAC CAA GTG ATG GAG GGG AAG AGT GCA ACC CTG ACC TGT GAG AGT Gly Asp Gln Val Met Glu Gly Lys Ser Ala Thr Leu Thr Cys Glu Ser 520 525 530	816
55		

	GAC GCC AAC CCT CCC GTC TCC CAC TAC ACC TGG TTT GAC TGG AAT AAC	864
	Asp Ala Asn Pro Pro Val Ser His Tyr Thr Trp Phe Asp Trp Asn Asn	
	535 540 545	
5	CAA AGC CTC CCC CAC CAC AGC CAG AAG CTG AGA TTG GAG CCG GTG AAG	912
	Gln Ser Leu Pro His His Ser Gln Lys Leu Arg Leu Glu Pro Val Lys	
	550 555 560	
10	GTC CAG CAC TCG GGT GCC TAC TGG TGC CAG GGG ACC AAC AGT GTG GGC	960
	Val Gln His Ser Gly Ala Tyr Trp Cys Gln Gly Thr Asn Ser Val Gly	
	565 570 575	
15	AAG GGC CGT TCG CCT CTC AGC ACC CTT ACT GTC TAC TAT AGC CCG GAG	1008
	Lys Gly Arg Ser Pro Leu Ser Thr Leu Thr Val Tyr Tyr Ser Pro Glu	
	580 585 590 595	
20	ACC ATC GGC AGG CGA GTG GCT GTG GGA CTC GGG TCC TGC CTC GCC ATC	1056
	Thr Ile Gly Arg Arg Val Ala Val Gly Leu Gly Ser Cys Leu Ala Ile	
	600 605 610	
25	CTC ATC CTG GCA ATC TGT GGG CTC AAG CTC CAG CGA CGT TGG AAG AGG	1104
	Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg	
	615 620 625	
30	ACA CAG AGC CAG CAG GGG CTT CAG GAG AAT TCC AGC GGC CAG AGC TTC	1152
	Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe	
	630 635 640	
35	TTT GTG AGG AAT AAA AAG GTT AGA AGG GCC CCC CTC TCT GAA GGC CCC	1200
	Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu Gly Pro	
	645 650 655	
40	CAC TCC CTG GGA TGC TAC AAT CCA ATG ATG GAA GAT GGC ATT AGC TAC	1248
	His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile Ser Tyr	
	660 665 670 675	
45	ACC ACC CTG CGC TTT CCC GAG ATG AAC ATA CCA CGA ACT GGA GAT GCA	1296
	Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly Asp Ala	
	680 685 690	
50	GAG TCC TCA GAG ATG CAG AGA CCT CCC CGG ACC TGC GAT GAC ACG GTC	1344
	Glu Ser Ser Glu Met Gln Arg Pro Pro Arg Thr Cys Asp Asp Thr Val	
	695 700 705	
55	ACT TAT TCA GCA TTG CAC AAG CGC CAA GTG GGC GAC TAT GAG AAC GTC	1392
	Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Asp Tyr Glu Asn Val	
	710 715 720	
60	ATT CCA GAT TTT CCA GAA GAT GAG GGG ATT CAT TAC TCA GAG CTG ATC	1440
	Ile Pro Asp Phe Pro Glu Asp Glu Gly Ile His Tyr Ser Glu Leu Ile	
	725 730 735	

CAG TTT GGG GTC GGG GAG CGG CCT CAG GCA CAA GAA AAT GTG GAC TAT 1488
 Gln Phe Gly Val Gly Glu Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr
 740 745 750 755
 6 GTG ATC CTC AAA CAT TGACACTGGA TGGGCTGCAG CAGAGGCACT GGGGGCAGCG 1543
 Val Ile Leu Lys His
 760
 10 GGGGCCAGGG AAGTCCCCGA GTTTCCTCCAG ACACCGCCAC ATGGCTTCCT CCTGCGTGCA 1603
 TGTGCGCACA CACACACACA CACGCACACA CACACACACA CACTCACTGC GGAGAACCTT 1663
 GTGCCTGGCT CAGAGCCAGT CTTTTTGGTG AGGGTAACCC CAAACCTCCA AAATCCTGC 1723
 15 CCTGTCTCTC TTCCACTCTC CTTGCTACCC AGAAATCATC TAAATACCTG CCCTGACATG 1783
 CACACCTCCC CTGCCCCACC AGCCCACTGG CCATCTCCAC CCGGAGCTGC TGTGTCCTCT 1843
 GGATCTGCTC GTCATTTTCC TTCCCTTCTC CATCTCTCTG GCCCTCTACC CCTGATCTGA 1903
 20 CATCCCCACT CACGAATATT ATGCCAGTT TCTGCCTCTG AGGGAAAGCC CAGAAAAGGA 1963
 CAGAAACGAA GTAGAAAGGG GCCCAGTCCT GGCCTGGCTT CTCCTTTGGA AGTGAGGCAT 2023
 25 TGCACGGGGA GACGTACGTA TCAGCGGCC CTTGACTCTG GGGACTCCGG GTTTGAGATG 2083
 GACACACTGG TGTGGATTAA CCTGCCAGGG AGACAGAGCT CACAATAAAA ATGGCTCAGA 2143
 TGCCACTTCA AAGAAAAAAA AAA 2166
 30

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 501 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Gln Val Glu Phe Leu Cys Met Ser Leu Ala Asn Pro Leu Pro Thr
 1 5 10 15
 45 Asn Tyr Thr Trp Tyr His Asn Gly Lys Glu Met Gln Gly Arg Thr Glu
 20 25 30
 Glu Lys Val His Ile Pro Lys Ile Leu Pro Trp His Ala Gly Thr Tyr
 35 40 45
 50 Ser Cys Val Ala Glu Asn Ile Leu Gly Thr Gly Gln Arg Gly Pro Gly
 50 55 60

55

	Ala	Glu	Leu	Asp	Val	Gln	Tyr	Pro	Pro	Lys	Lys	Val	Thr	Thr	Val	Ile	
	65					70					75					80	
5	Gln	Asn	Pro	Met	Pro	Ile	Arg	Glu	Gly	Asp	Thr	Val	Thr	Leu	Ser	Cys	
					85					90					95		
	Asn	Tyr	Asn	Ser	Ser	Asn	Pro	Ser	Val	Thr	Arg	Tyr	Glu	Trp	Lys	Pro	
				100					105					110			
10	His	Gly	Ala	Trp	Glu	Glu	Pro	Ser	Leu	Gly	Val	Leu	Lys	Ile	Gln	Asn	
		115					120						125				
	Val	Gly	Trp	Asp	Asn	Thr	Thr	Ile	Ala	Cys	Ala	Arg	Cys	Asn	Ser	Trp	
15		130					135					140					
	Cys	Ser	Trp	Ala	Ser	Pro	Val	Ala	Leu	Asn	Val	Gln	Tyr	Ala	Pro	Arg	
	145					150					155					160	
20	Asp	Val	Arg	Val	Arg	Lys	Ile	Lys	Pro	Leu	Ser	Glu	Ile	His	Ser	Gly	
					165					170					175		
	Asn	Ser	Val	Ser	Leu	Gln	Cys	Asp	Phe	Ser	Ser	Ser	His	Pro	Lys	Glu	
					180				185					190			
25	Val	Gln	Phe	Phe	Trp	Glu	Lys	Asn	Gly	Arg	Leu	Leu	Gly	Lys	Glu	Ser	
		195					200						205				
	Gln	Leu	Asn	Phe	Asp	Ser	Ile	Ser	Pro	Glu	Asp	Ala	Gly	Ser	Tyr	Ser	
		210					215					220					
30	Cys	Trp	Val	Asn	Asn	Ser	Ile	Gly	Gln	Thr	Ala	Ser	Lys	Ala	Trp	Thr	
	225					230					235					240	
	Leu	Glu	Val	Leu	Tyr	Ala	Pro	Arg	Arg	Leu	Arg	Val	Ser	Met	Ser	Pro	
35					245				250					255			
	Gly	Asp	Gln	Val	Met	Glu	Gly	Lys	Ser	Ala	Thr	Leu	Thr	Cys	Glu	Ser	
					260				265					270			
40	Asp	Ala	Asn	Pro	Pro	Val	Ser	His	Tyr	Thr	Trp	Phe	Asp	Trp	Asn	Asn	
		275					280					285					
	Gln	Ser	Leu	Pro	His	His	Ser	Gln	Lys	Leu	Arg	Leu	Glu	Pro	Val	Lys	
		290					295					300					
45	Val	Gln	His	Ser	Gly	Ala	Tyr	Trp	Cys	Gln	Gly	Thr	Asn	Ser	Val	Gly	
	305					310					315					320	
	Lys	Gly	Arg	Ser	Pro	Leu	Ser	Thr	Leu	Thr	Val	Tyr	Tyr	Ser	Pro	Glu	
					325				330					335			
50	Thr	Ile	Gly	Arg	Arg	Val	Ala	Val	Gly	Leu	Gly	Ser	Cys	Leu	Ala	Ile	
					340				345					350			

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Leu Ile Leu Ala Ile Cys Gly Leu Lys Leu Gln Arg Arg Trp Lys Arg
 355 360 365
 5 Thr Gln Ser Gln Gln Gly Leu Gln Glu Asn Ser Ser Gly Gln Ser Phe
 370 375 380
 Phe Val Arg Asn Lys Lys Val Arg Arg Ala Pro Leu Ser Glu Gly Pro
 385 390 395 400
 10 His Ser Leu Gly Cys Tyr Asn Pro Met Met Glu Asp Gly Ile Ser Tyr
 405 410 415
 Thr Thr Leu Arg Phe Pro Glu Met Asn Ile Pro Arg Thr Gly Asp Ala
 420 425 430
 15 Glu Ser Ser Glu Met Gln Arg Pro Pro Arg Thr Cys Asp Asp Thr Val
 435 440 445
 Thr Tyr Ser Ala Leu His Lys Arg Gln Val Gly Asp Tyr Glu Asn Val
 450 455 460
 20 Ile Pro Asp Phe Pro Glu Asp Glu Gly Ile His Tyr Ser Glu Leu Ile
 465 470 475 480
 Gln Phe Gly Val Gly Glu Arg Pro Gln Ala Gln Glu Asn Val Asp Tyr
 485 490 495
 25 Val Ile Leu Lys His
 500

30 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Arg Gly Asp Arg Ala Glu
1 5

45

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Pro Glu Ser Thr

1

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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

15

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

25

Leu Ala Thr Asp Met Ser Cys His Phe Gln Gln Val Lys Thr Met Lys
1 5 10 15

Thr Ala Leu Gln Gln Leu Glu Arg Ile Asp Lys Ser Lys Ala Leu Ser
20 25 30

30

Leu Leu Leu His Ala Ala Asp Ile Ser His Pro Thr Lys Gln Trp Ser
35 40 45

Trp His Ser Arg Trp Thr Lys Ala Leu Met
50 55

35

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

50

Ile Val Phe Ser Ala Cys Arg Met Pro Pro Ser His Gln Leu Asp His
1 5 10 15

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Ser Lys Leu Leu Gly Tyr Leu Lys His Thr Leu Asp Gln Tyr Val Glu
 20 25 30
 6 Ser Asp Tyr Thr Leu Leu Tyr Leu His His Gly Leu Thr Ser Asp Asn
 35 40 45
 Lys Pro Ser Leu Ser Trp Leu Arg Asp Ala Tyr Arg Glu Phe Asp Arg
 50 55 60
 10 Lys Tyr Lys Lys Asn Ile Lys Ala Leu Tyr Ile Val His Pro Thr Met
 65 70 75 80
 Phe Ile Lys Thr Leu Leu Ile Leu Phe Lys Pro Leu Ile Ser Phe Lys
 85 90 95
 Phe Gly Gln Lys Ile Phe Tyr Val Asn Tyr Leu Ser Glu Leu Ser Glu
 100 105 110
 20 His Val Lys Leu Glu Gln Leu Gly Ile Pro Arg Gln Val
 115 120 125
 25

Claims

1. A nucleic acid molecule that encodes a polypeptide which binds to a site of a molecule which regulates cell survival, wherein said nucleic acid molecule comprises:
 - (a) the nucleic acid sequence shown in SEQ ID NO: 20;
 - (b) the coding region of the nucleic acid sequence shown in SEQ ID NO: 20;
 - (c) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 21;
 - (d) the nucleic acid sequence shown in SEQ ID NO: 22;
 - (e) the coding region of the nucleic acid sequence shown in SEQ ID NO: 22;
 - (f) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 23;
 - (g) the nucleic acid sequence shown in SEQ ID NO: 24;
 - (h) the coding region of the nucleic acid sequence shown in SEQ ID NO: 24;
 - (i) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 25;
 - (j) the nucleic acid sequence shown in SEQ ID NO: 26;
 - (k) the coding region of the nucleic acid sequence shown in SEQ ID NO: 26;
 - (l) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 27;
 - (m) the nucleic acid sequence shown in SEQ ID NO: 28;
 - (n) the coding region of the nucleic acid sequence shown in SEQ ID NO: 28;
 - (o) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 29;
 - (p) the nucleic acid sequence shown in SEQ ID NO: 30;
 - (q) the coding region of the nucleic acid sequence shown in SEQ ID NO: 30;
 - (r) a nucleic acid sequence which encodes the amino acid sequence shown in SEQ ID NO: 31; or
 - (s) a nucleic acid sequence which hybridizes to any one of (a) to (r).
2. The nucleic acid molecule of claim 1, wherein said site is fifteen amino acids or less in size.
3. The nucleic acid molecule of claim 1, wherein said site is ten amino acids or less in size.
4. The nucleic acid molecule of any one of claims 1 to 3, wherein said site is SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, or SEQ ID NO:32.
5. The nucleic acid molecule of any one of claims 1 to 4 which is a DNA molecule.

6. A vector comprising the DNA molecule of claim 5.
7. The vector of claim 6 wherein said DNA molecule is operably linked to a promoter.
- 5 8. A host cell transformed with the vector of claim 7 or 8.
9. A method of producing a polypeptide which binds to a site of a molecule which regulates cell survival, comprising:
 - (a) culturing the host cell of claim 8; and
 - 10 (b) recovering the polypeptide expressed by the host cell.
10. A polypeptide which binds to a site of a molecule which regulates cell survival produced by the method of claim 7 or encoded by the nucleic acid molecule of any one of claims 1 to 5.
- 15 11. The polypeptide of claim 10, having the amino acid sequence of SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29 or SEQ ID NO:31.
12. A nucleic acid molecule that encodes the site of a molecule which regulates cell survival to which the polypeptide of claim 10 or 11 binds.
- 20 13. A pharmaceutical composition comprising the nucleic acid molecule of any one of claims 1 to 5 or 12; the polypeptide of claim 10 or 11; or an oligopeptide encoded by the nucleic acid molecule of claim 12; and, optionally, a pharmaceutically acceptable carrier.
- 25 14. A diagnostic composition comprising the nucleic acid molecule of any one of claims 1 to 5 or 12; the polypeptide of claim 10 or 11; or an oligopeptide encoded by the nucleic acid molecule of claim 12.
15. Use of the pharmaceutical composition of claim 13 for the preparation of a medicament for regulating cell death, neutralizing activity of a molecule which regulates cell survival, treating or ameliorating immune disorders, or treating or ameliorating abnormal states characterized by aberrant cell growth.
- 30 16. A method for regulating cell death in vitro comprising exposing said cell to the polypeptide of claim 10 or 11.
17. A method for neutralizing activity of a molecule which regulates cell survival in vitro comprising exposing a cell to the polypeptide of claim 10 or 11.
- 35 18. The method of claim 17, wherein said molecule which regulates cell survival is Bcl-2.
19. The method of any one of claims 16 to 18, wherein said cell is exposed to said polypeptide by transfecting said cell with the nucleic acid molecule of any one of claims 1 to 5.
- 40 20. A method for identifying a molecule which regulates cell survival, comprising:
 - (a) lysing cells suspected of comprising a molecule which regulates cell survival to produce a lysate;
 - 45 (b) exposing said lysate to the polypeptide of claim 10 or 11; and
 - (c) determining the presense of molecule-polypeptide aggregates.

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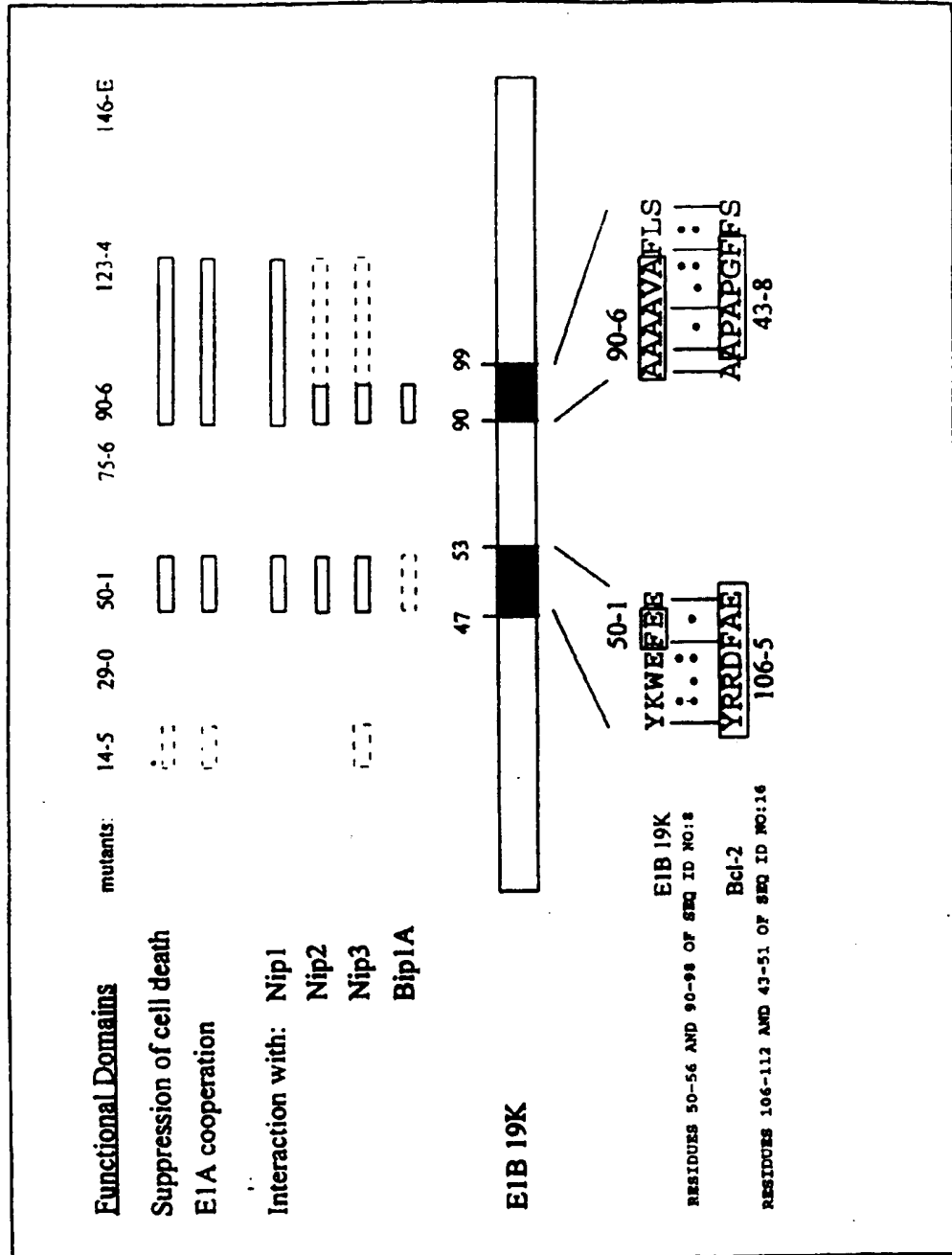


FIGURE 1

A. Nip1 43 Intkvkekfgqlrhrifqdlleqlakeqkesekqlllq...evenhkkqmlsnqaswrkanl 100 RESIDUES 43-100 OF SEQ ID NO:21
 Nip2 79 LATDMSCHFQQVKTMTALQQLERI.DKSKALSLLLHAADISHPTKQ.WSWHSRWTKALM 388 SEQ ID NO:34
 CaM-PDE 331

B. Consensus O * O * O G * * O * * E
 Nip2 79 E I P L D G L D T P S E 90 RESIDUES 79-90 OF SEQ ID NO:23

C. 168 vvfavcfcmpessqpnyrylmdnlfkyyvigtellellvaenymivylngatttrrkmpslgwlrkcyqqi 233
 86 IVFSACRMPPSHQLDH....SKLLGYLKHHTLDOQYVESDYTLLYLHHGLTSDNKPSSLWLRDAYREF 147
 234 drrlrknklslllvhpswfrtlllavtrpfisskfsqkiryvfnlaelaelpmeyiqipeckqv 299 RESIDUES 168-299 OF SEQ ID NO:23
 148 DRKYKKNIKALYIVHPTMFIKTLLILFKPLISFKFGQKIFYVNVYLSLSESEHVKLEQLGIP...RQV 210 SEQ ID NO:35

FIGURE 2